

CGACGCGTGGGTGCGAGGCCAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
CCTGGTGCACCCACCACT**ATG**TTGGCTGCAAGGCGTGGTGTCTCCGAGCACTACCTTCTAGG
GTTTCCACCACCGAGTTTCAGTCCAGCTCCCTCTGTGTGAAGAATTCCATCAACAGAATCA
ATGGCTGTTAAACCTAGCAGGGAATATGCCACCAAAACAAGAAATTGGGATCCGGCGTGGGA
GAACCTGGCCAAAGAACTCAAGAGCGCAGCATTTGGAACCTCGATGTGAAAAAATATTAAAAAT
GATCAGATGGGGAAGATGTTTGTGCTGAGGGGCTGCTGTTGGCTCTGGAGCATTTGTGCTA
CTATGGCTTGGGACTTCTAATGAGATTGGACGTTGCAAAAGGCTGTAATTTGGCCTCAGT
ATGTCAAGATAGAATTCTATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
TTGTCTGCCATAGCAATCAGCAAGACGCTGTGTTCTATGAACCTCATGATGAGAGGCTCTTG
GGTGCAAAATTTGGTGTGACCTTTTGACGCCATGGTTTGGAGCTGGAATCTGGTGACATCAATAC
CATATGACGACAGCCGAGGCCCAAAAGCATCTTGGTTGGTGACTACTCTGGTGTGATGGGT
GCAGTGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
AGCTGGCATCTGGGAGGCCCTCAGGCTGTGGCCATGTGTGCGCCAGTGAAAAGTTCTTGA
ACATGGGTGACCCCTGGGAGTGGGCTTGGCTCTGCTCTTGTGTCCTCATTTGGGATCTTGA
TTTCTTCCACCTACCACCGTGCTGTGTGCCACTCTTTCATCAGTGGCAAGTGTACGGTGGAAT
AGTCTTTTTCAGCATGTTCCCTGTGTATGATACCCAGAAGTAATCAAGCTGCGAGAATAT
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
ACATTAATAATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAAGAA**TG**
AGTGATCAGCTTCTTGCTTCTCTGCTACATCAAATATCTGTTTAATGGGCGAGATATGC
ATTAATAGTTTGTACAAGCAGCTTTCTGTGAAGTTTAGAAGATAAGAAACATGTCATCATA
TTTAAATGTTCCCGGAATATGTGATGCCTCAGGCTGCTCTTTTTTCTGGAGATAAATGCAAT
AATCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAAGTATTTTAAAAATGTT
TTGGTGAAATGTGAAAACTAAAGTTTGTGTCATGAGAAATGAAGTCTTTTCTACTTTAAAA
TTTAGTAGGTTACTGATGATACTAAATTTAGCAAACTGTGTTTGGCATATTTTGGAGT
GCAGAAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGACCAGAGAGAAG
GAGTCACTCGAGCTCTTTGTTTTTAAATACATAGAACTTAGCATTGCTGTTTATGATTA
GTAGGAGCGCAGTAAGAAAGCTCTGGGATTTGGAAACAAGTGTCATTGTTACATTCATTT
GCTGAACTTAACAAAACCTGTTTCATCTGAAACAGGCACAGGTGATGCATCTCTCTGCTGTG
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCTATGTTGACTTGTACAGAAATGTAATC
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTGAATGTTACAAAAGGAA
ATAACTTTTAAACATATTTCTACAGAGAAAATATTCAAAAGCATGAAATATGTTGCTTTTCCAG
AATACAAACAGTACTATCATG

MLAARLVCLRTLPSRVFHPAFTKASPVVKNISITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRFVAVAGGAAGLGCYYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMMFMRGWSVTIGTVFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLIGGLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
VGLGLVLVFSLSGSMFLPTTVAGATLVSAMYGGLVLFMSFLLYDQKVIKRAEVSPMYGV
QKYDEINSMLSIYMDTLTIFMRVATMLATGNGRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCGCCGCTCTCGCGCTTCTGCAT
 CGCGGCTTCGGCGGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGCTCGTGAGG
 GGTCCGGCAGCGGGAGTCGGCGGCTTGTGCATCTTGGGTACCTGTGGGTCCGAAG**ATGTC**CGG
 ACATCCGAGACTGGTTTCAGGAGCATCCCGCGCATCACGCCGCTATTGGTTCCGCCGCCACCTC
 CGCGTGGCTTTGGTCGGCAAACTCGGCCTCATACGCCCGGCCTACCTCTCCCTCTGGCCCGA
 AGCCTCTCCCTTATCGCTTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 TCCAGGAATCGGATTTCTTTATTTGGTCAATTTATATTTCTTATCAGTATTTACGCGCA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCTCTGTATCA
 TGTCACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTGGGA
 ACACGATTTAAGGCCCTGCTATTTACCCTGGGTATCCCTGGATTCAACTATATCATCGGAGG
 CTCGGTAAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCA
 GATACCAATGGACTTTGGGAGGAAGAATTTCTATCCACACCTCAGTTTGTTCACCGCTGG
 CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCTCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGAGGCGGGAGACACAAC**TGGGGCCAGGGCTTT**CCAGCTGGAGACC
 AG**TGA**AGGGGGCGGCTCGGGCAGCGCTCTCTCAAGCCACATTTCTCCCACTGCTGGGTG
 CACTTAACAACCTGCGTTCGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAGAGTCTTTAAATCCCGAAGAAAAATAAGTGTTCACAAGTTTCACGAT
 TCTCATTCCAAGTCTTACTGCTGTGAAGAACAAAATACCAACTGTCGAATTTGCAAACTGAC
 TACATTTTGGTGTCTCTCTCTCCCTTTCCGCTCTGAATAATGGTTTTCAGCGGTCCCT
 AATCTGCTGGCATTTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGCACACATGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCACTAGAAAAAGTCTG
 CCCATAAAATTTGCTGCGCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGTC
 ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGCCAGCGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGCATCCGTTGTT
 AACCGTTTGCCACTCTTCAGATATTTTATAAAAAAGTACCACCTGAGTTTCATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACGAGGGTTGGTGTGGGTGTTTGGTTCTGAGCTAAGTGA
 TCAAGACTGTAGTGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGGGGATGCCACCC
 TTTGCGTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGATGTTGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCTATG
 ATTTCCATTTCAATCTCATTCTGGATATGTTCTCATTGAGTAAGGAGGAGAGACCCATGA
 CGCTATTTAAATGTCACTTTTGGCTATCCCCGTTTTTTGGTCACTGTTTCAATTAATGTT
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAAGCACATCTA
 AGGGAATAACATGATTTAAGGTGAATGGCTTTAGAATCATTGGGTTTGAGGTTGTGTTA
 TTTTGAGTCAATGAATGTACAGCTCTGTGAATCAGACAGCTTAAATACCCACACCTTTT
 TCGTAGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCA
 TGGCTTTTCCACAGTTTATTTTATTTATGACGTTATCTGAAAGGACACTGTTAGGAGCAGT
 ATTGAGTGGCTGTACACACTTTGAGGCACTAAAAAGGCTTCAACACTTTTGTATCAGTTCTCT
 TTCCAGGAACATTTGGCTTAACAGTATGACTATTTCTTCCCCACTCTTAAACAGCTGTGAT
 GTGTGTTATCTAGGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTGTGTG
 TACTTCTCCATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA
 TGTTTTGTGTTTCTATCTGTGGCCACATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
 CCAATTATGTTGCAGTACACTCATTGTACGGCTGGAGACTCATTGTATGTATAAGGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCTCTTACCAGTCAAGTGCCTGCGAG
 CAGTCATTTTTTTCTAAAGGTTTACAAGTATTTAGAATTTTCAGTTTCAGGGCAAAATGTTT
 ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTTGATTGTCTGGATT
 ATGTTTCTGGAATTTTATTTACCAAAACAAGCTATTGAGTTTGTACTTGACAAGGCCAAACA
 TGACAGTGGATTCTCTTACAATGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTAAACTAATCTTTTATTTGGTAAAAATGTAAATTAATGTGCACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTGT
GTAGCTTCTATCTCTGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCTAACCGGGGTCGGCGGTCTGGCTTAGGGATCTTCCCCGTTGCC
CCTTTGGGGCGGGATGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCTCGCAGGCCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGAATT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCTCTTGCAAAGACCCATACATCACAGGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAACCGATGGCTCTGATGTGCTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCTCCTCTC
CACAAAAGGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
TTATCAGTACTTTGGAACAGAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
TAAGTGTGATGTCATCAGGAAGAAGTATGAGGACTAAACAGATACAAAATATTGGAGCAGAAAG
GAAAACCATCTGGGGAGGTAGAGGAATGACAGAGAAACAGAAATGACAGCAGAGGAGAAG
CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGCTA
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGCTTTAAAAATAAATATTTAGTCT
CTTACACTG

FIGURE 6

MAAEEDDEVWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEESKLTYTEIHQYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTAGAAAGGTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

CGTGGTTTTTGTCTCGCAATAGCGCGCTTAGAGGGAGGGGCTTTTCGCTATACCTACTG
TAGCTTTCTCCAGCTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTACTG
TCTCAGCTCTAGGATGTCGCTTCTCCACTAAGAGCTCTTCTAGGGAGGTAATTAATAAAC
AGTGGAAATGGAAGAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC
ATTCCTGCTAGGTGCCATATTCATGCTTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTAT
TCTGCAATAGAGAAACAAAGATGATTATCTTCCAACACTGCTGGAATGCTGCTCAGAAGCTG
GTGAAGCTAGTTTTTCTGTGCTGTGTGTCATCTCTGTGTTATAAGAAAGATCATCAAGTAG
AAATTTGAAATATGCTTCTCGGAAGGAATTCCTGTGATTCATGAAGTGGTCCATTCCTGCC
TTCTTTATTTCTCGGATAACTTGATGTCTCTATGCTCTGCTATCTTCAACAGGCATG
GCTGTATCTTCTCAAAATTTAGCATTTATAACAACAGCTCTTCTATTTCAGGATAGTGTCTGAA
GAGGCGCTAAACTGGATCCAGTGGGCTCCCTGACTTTTATTTTGTCTATTGTGGCCT
TGACTGCCGGGACTAAAACTTTACAGCACAACTTGGCAGGACGTGGATTCATCAGCATGCC
TTTTTCAGCCCTTCCAATTTCTGCTCTCTTTTCAAGAAGTGATGCCACGAGAAAGACAAATTG
TACAGCAAGGAATGGACTTTTTCTGAAGCTAAATGGAACACCAAGCCAGGAACTTTCAGTC
ACATCCGCTTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT
AATATCTATAAATGAAAGATATCGAAGGAGGGAACAGCTCACTGAAGACATCTTCATACA
GAACAGCAAATCTATTTCTTTGGCACTCTGTTTTAATGGGCTGACCTGGGCCCTCAGAGGA
GTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
CTTATTTTGTAACTGCAATCCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGTAA
CATGTTCATGTCTTGATGGCCAGGTTACCACTGTCTATTATCACAGAGTGTCTGTCTGG
TCTTTGACTTCAGGCCCTCCTGGAAATTTTTCTTGGAAAGCCCATCATGCTCTCTCTCTATA
TTTATTTAATGCGCAGCAAGCTCAAGTTCCGGAATACGCACCTAGGCAGAAAGGATCCG
AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGAGTGGAAGAAGACTAGAAGACTTA
CAAAACCCAAAGATGATGAGTCAGATGAAGATACTTCTTAACCTGGTACCCACATAGTTTGC
GCTCTCTTGAACCTTATTTTTCATATTTTTCAGTTTGTGAATATTATCTTTTCTCATTTGATA
AACCAGAAATGTTTCTAAATCCTAATATTTCTTGCATATATCTAGCTACTCCCTAAATGGTT
CCATCGAAGGCTTAGAGTCCCAAAAGGCTAAGAATAATCAAGAAGCTGATACAGGATGAACA
ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCGAAAGTATATATGTGCAGATTAT
TTTCCTTGGCCTTCAAGCTTCCAAAAAATCTGTAATATCATGTTAGCTATAGCTTGTATAT
ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
CTTCCCTTTTACATATATAAAGCTAGGTTGTCTCTGAATTTTGAAGGCCCTAGAGATAGT
CATTTTGAAGTAAAGAGCAACGGGACGCTTCTAAAGAACTGGTGTGAAGGCCATTAATAT
CTGGCCACCATTAAGATTTGGGATGATGTAGTCTGTGCTGAATATTTTGTCTGAAGACAGT
TTCTCAGACACAACATCTCAGAAATTTTAATTTTGAAGAAATTCAGGAAATTTGGATTTTGT
AATAATCTTTTGATGTTTAAACATTTGGTTCCTGATGACCATAGTTTACCACTGTATTTTA
AGTCAATTTAAACAGGCAGGTGGGGCTTTTTCTCTCAGTTTGAAGGAAAAATCTTGAT
GTCATTACTCCTGAATTTATTCATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
AATTCAGCTGTGACTATTGTATATCTTTCCAAGTGTGAATCTGGCTTCAGATCATAC
CAGATTGTGTCAGTAGAGCTGATGCCTAGGAATTTTAAAGGACTCTTCAAAAGGATCACTT
AGCAAAACACATGTTGACTTTTACAGTATGATGAATATTAATACTCTAAAAATGAAAGACC
AGTAATATAAGTCACTTTTACAGTGCTACTTCACACTTAAAGTGCATGGATTTTTCATG
GTATTTTGCATGCAGCGAGTTAACTCTGTGATAGAGAAGTCAGGTGATAGATGATATTA
AAATTAGCAAAACAAAGTGACTGTCTCAGGGTATGCAGCTGGGTGATGATAGAAAGTGGG
CTTTTACGTCAGGCGCTGTATGTTTACAGACTACCACTACTGTAATATGACTTTATGTGT
CATTTCTCAGAACTTATACATTTCTGCTCTCTTCTCTCAAGTTTCATGCAGATGATATA
AGGTAATATCTATTATATAATTCATTTGCTGATATCCAAATAATATGACTGGCAAGAAATG
GTGGAATTTTGAATTTAAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFNSFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITT VSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDL SGNLWERSSSGDGEELERLT KPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTC TGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGCTCAA
CTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCGAGGAGCAT
 CCCGCTCTACCAAGTCCCAAGCGGCGTGGCCGCGGGTCTATGGCCAAAGGAGAAGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCTGGGTTTCTTCCTTCAGATCTAC
 CTATTG**CATG**TGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCAGACGCCCTGGTGGGCTCTGCATCAGCAAAATCCCCCTGGACCTGCC
 TGGTTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGCTATTGCGCTACTTCCCT
 ATCTGGTTCGTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCTATCGGATGACTGTGGAAGTGTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCAAGCAGACACGCCCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAAACCATACACATGGCACCACTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTATCCTGATCCTGGGCGTGCAGGAGCAGAGAGAACCCATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCTATGAGCCAGGCCCATACATCAAACCT
 ATTACTGGCTTCCTCTTCACTCCTTGGCTTTTCATGCTGGTGGAGGGAACTTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTCCTCATCTGGCAGTGGTTCTTGACCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATCGGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTATGTCTTCTTCAACAAGTTTGCTCTGGAGTGTG
 ACTGGGCATTTTCAACCCTCAGTCTGGACTTTGACGGGTACAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAAATGTACCCCATGATGAGGAGAGGCGGCGGAGAAATAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGTGGCTAGCATCCTC**TAGG**GGCCCGCCACGTTGCCGGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCGGCTTGTCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGAGGTGGCCAGGACACTTGTGTCTCACTGTGGGCGCGCTGCTCTG
 TGGCCTCCTGCCTCCCCCTGCTGCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAGCTGGAAGC

00000000 10001 10001 10001

FIGURE 12

MWLRWALSLPPSSCLWAEPMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFISIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVICIYIICAV
ILILGVREQREPYEAAQQSEPIAYFRGLRLVM SHGPYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

100241-5626860

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACTTTGTCCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCCTGCGCAGTGGTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

CCCTTGGTCCATGCTGCCTGATGTGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCGTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTCGGTCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGAGAAAAATCAGCGGTCTAATTAAATCTCTGTTTGTGTAAGCAGT
TACCAAGAATCTCAACCTTTCCCAACAAAAGCTAATTGAGTACAGTTCCTGTTGAGTACA
CGTTCTCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTGCTGTAACACAGAAACCTGTTAGAAATGTGGTGGTTTCAGCAGGCGCTTACTGTTCCCTTCT
TTCAGCCCTTGAATTTGGACATCTGCTGCTTCATATTTTCATACCTTACTGTCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATACAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCGCCGTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGG
 CCGGGGTGCGGAGCCGAC**ATG**CGCCCGCTTCTCGGCCTCCTTCTGTGCTTTCGCGGCTGCAC
 CTTTCGCTTGTACTTGTCTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCTTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTATTAATAAATTT
 AGTCAGAAACATCTGCAATGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACAT**TGA**CTCGGATTTTCTGTTTGCCACATCCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTTGCTCCTTAAAGCCCCCTCATTTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCAGGCCGGTGATTCT
 ACAAGGTCAAGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRRLPRGRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
 KEHQAYVFLFCGAYLYKQGFATPGSSFLNVLGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPDPKVALLRKVEENRNSLFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLGAHTWRSIIHHIRLMSLP IAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPFPYPWRRPLNRSQMLRELFVP
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGCGGCAGCTGTCCCCGAGCGGGAGGAGCCCCAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTCCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAACAGCTCAGAACAGGAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAGAATGAACCTCAGAGACCCCCCGAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTCTGGTGGTG
 CCCTGTTGGCCACGCTGCTAGACCGTGCTTATGAGCGCTGGGGCTGCAGTGGGACCTGCC
 CTCCTCGCCACCCCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGCTTTTGTGGCCA
 ACCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACTGTCAGATTTCGAATG
 GACACGTTATGCTAAGAGCCAGACCTTATGTCAAGTTTCTGGAATGCTCTATGACATGCT
 TATGAGCAGTGGGACGGCGCCAGTGGGAGCGCCGACAGTCTGTCGGGCTCTCCAGGAGC
 TGGTGTCTGGAACCTGCGCAGAGGGCGGGCGCGCTGGAGGGGTACGCTACACGGCAGTCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGCGCTGTGGCGCCAGCT
 CGGCCAGCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA
 GCGCCGAGACATATTCACGCATCGCTCTGAAGCTGGTGCCCAACCATCAGTTCGACCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCTCTGACACCCACCGGAGGCG
 CTCACTGCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCAGTGTCTGCAGG
 AGGACCACTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGACGAGAAGT
 GATGAGCAGCGTGAGAAGCTGGTGTCTGCGCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCCAGGGCTGCTGGAGGTACACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCGATCGGCTATGATTTCCGCGGCCACTGGCCAGCTCGGTGAG
 GTCCACTCTGCGGGCTTTCAACTGCGCCGTTCAGCACTTGAGCTTCTCTTATCGATCAGGC
 CAACTACTTCTCAACTTCCATGCAAGGTGGGCGACGACCCAGTCTCAGTCTCTAGCCAGA
 CTCGAGACCCCACTGCGGCCATCCACCCCATACCAGGTACGGAACCAAGTGTATCTCG
 TGCTCTCTGGCCTAGCCGCCCTCTCAAGGCTACCTAAGCAGGCGCTCCCCAGGAGAT
 GCTGCGTGCCTCAGGCCTTACCAGAAATGGGTACAGCGTGAGATATCCAATCTCGAGTACT
 TGATGCACTCAACACCATTTGCGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTCT
 CCCTGGGTCTGTGAGGACTACGTGTCCCAACCTGGACCTCAGCAACCCAGCGCTCTCCG
 GGACCTCTTAAGCCCATCGGTGTGGTGAACCCCAAGCATGGCCAGCTCGTGAGGGAGAAGT
 ATGAAAGCTTTGAGAGCCAGCAGGAGGACATTGACAAGTTCCACTATGGCACCCACTACTCC
 AATGACGAGCGGTGATGCACTACCTCATCCGCGTGGAGCCCTTCACTTCCCTCAGCTGCCA
 GCTGCAAGTGGCCGCTTTGACTGCTCCGACCGGCGAGTTCCTCTCGTGGCGGCGAGCTGGC
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCGGAATTTCTTACTTTCTCT
 GACTTCTTGAGAACCCAGAACGGTTTTGACCTGGGCTGTCTCCAGTGTACCAACGAGGAAGGT
 AGGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCTGAGGACTTATCCAGCAGCACCGCC
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACCTACACGAGTGGATTCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCGAGCCGCGGAGGAGGCCCTCAATGTCTTATTATGCACTTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTGA
 TCAGCAACTTTGGGCACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAATCGGCTCTCA
 GCTGGAGGAAGCAGCCCATCGCCTTGACAGCTTGACACTAATCACTACGATCTTCAGCA
 CCTGGAGCAACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGCCAGTGGGCTGTCTGGGA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAAGCTTCAGCAAGAGCCCC
 ACCATGGGAGGCCAAGACGACGAGCACTGCTGAGTGCCCTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTCAAGCGGTGGCCACTGGG
 ATGGCTCTGGGTGACTGCACTACCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCCTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACTGCTGGTGTGGCGGCTCTGTCATCAGGTGGTCTGTGACTAGGCTGAGC
 CAAAGCCTGTGAGGTCTGTATGGGCACTGGGCGTGCAGTGAAGTGTGTGGCCATCAGCAT
 GAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAATGTGATCATACACATGTACCGG
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTCACCC
 TGGCATTTGGGTGCAAGGCGAGATTGTGGTACAGAGCTCAGCGCTGGGAACCTCTTGGGCC
 CAGGTACCTACTCTTGCACCTGTATTCAGTCAATGGGAAGTGTGGGGCTTCACTGCCCTCT
 GCGAGACGCTGCTGACGGTACGGTGACAGGAGACTTTGTGTTCTGGGCAAGCCGCGAGT
 GCGCCCTGACATCTCTCAACTAAACACACTGCTCCCGGCCGCGCTCTCTTGGCCATGAAG
 GTGGCCATCGCCAGGTGGCGCTGACCAAGGAGCGCAGCCAGTGTGGTGGGCTGGAGGA
 TGCGAAGCTCATCGTGGTGGTGGCGGGGACGCCCTGTGAGGTGGCGAGCAGGAGTTGCGCG
 GGAAGCTGTGGCGGTCTCTGCGGCGCATCTCCAGGTCTCTCGGAGAGACGGAATACAAC
 CCTACTGAGGCGCGCTGAAGCTGGCCAGTCCGGCTGCTCGGGGCCCGCCCGGCGAGGCCTG
 GCGCGGAGGCCCCCGCCAGAAGTGGCGGGAACACCCCGGGTGGGCGCCAGGCGGTGA
 GCGGGGCCACCTCTGCCAGCTCAGGAGTTGGCGGGCGATGTTACCCCTCAGGAGTTGGCG
 GCGCGAAGTCCCGCCCTCGCGCGCTGAGGGCCGCCCTGAGGGCCAGCACTGGCGTCT

03666293 412066
 100211 66268650

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCAT
CCAAAGGCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATATGGGCTCCTGGGCTCTTC
TGGACCCTTAAGTGGTACTGGCCCTGGGGCAATGCGTCTCGCTGAGCCCTTGCTCTCTT
CTACTGGGCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTTGGAGCCCTCATCCTGACCTTGTGCAG
ATAGCCCGGGTCACTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
CCGCTGCATCATGTGCTGTTCAAGTGCTGCCTCTGGTGTCTGAAAAAATTTATCAAGTTCC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGATAATCTGTCTCTCAGCCAA
AATGCGTTCACTGTCATCATGCGAAACATTTGTCAGGGTGGTCTGCTGGACAAGATGCACAGA
CCTGCTGCTGTCTTTGGGAAGCTGCTGGTGGTGCAGGCGTGGGGTCTCTGTCTCTCTTT
TTTTCTCCGGTCGATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTTGGGAAGACCTGGAGCGGAACAAC
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGAGCTCCGGCCCTGATCCAGGACTGC
ACCCACACCCACCGTCCAGGCATCCAACCTCACTTCGCTTACAGGTCTCCATTGTGTGGT
AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCAGGCCTGAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCTCC
GTCCTATTAAAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
TCGGCGCACTGCATCCCACTCGGTCGGTGACAGACTCTGTCTCCAAACAAAACAAACAA
AAGATTTTTATTAAGATAATTTGTTAACCTC

RTRGTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCFVQGYSSKGLIQRSVFNLIQYGVGLGF
WTLNVWLALGQCVLGAFASFYWAHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLGRGVQNPVARCIMCCFKCLWLEKFIKFLNRNAYIMIAIYGNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSLILGAYIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKK
EAPDNNKKKK

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCCGCGCT
GGCTA**TG**TTTCGTGTCCGATTATCCGCAAGAGTTCACGAGGTGGTCCAGAGCCAGAGGGTCC
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTG
CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
ACCTATTGGATATCTTCAACCTGATGAAGACATATATTCTTTGTGTGTGACTCCCATAGG
CCAGTCAATGTCTCAATGTATACAACGATACCCAGATCAAATTACTTCATTAAACAAGATGA
TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
CAGGAAATGACAGTGTGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
GTGGAGCAAAACCATGCGGAGGAGGCAGCGCGCAGAGTGGGAGGCCCGGAGAAGAGACATCTCT
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
CAGTGGGTGCAAGACAGATCACTCAAAATGAAATACGTGACTGATGTGTGGTGCTCTGCAGCG
CCACGTTTCCCGCCACAAACCAGCCGGAAGGAGATGAGGAGAACAACACTCTCCCTGGACTGCA
CACGATCTCCTTTGAGTATGACCTTCGCGCTGGTGCTCTACACAGCATGGTGCTCTCATGAC
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
TTTGGGATGAAGGACATGCGCGTGCAGACTTTGACGATTCATTTTGGGTTCAGCACAAAGTT
TCTGGCCAGCGAGCTGGTCTTTGCCACCATGCTTTGATGGAGAGCCCCGAGAAGGATGGCT
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTCTGTACTGCTCTCTCATGGAGGGCAC
TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAAACCTGCTCA
AGTCCCTTGTGTGTTGCAAAAAGAACCGCGCTGCAAACTGCTGCCCTGGTGATGGCTGCC
CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAAGCTCCCGGA
TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
CTGAGCAACTGTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCAGAATGACCTTCTTATT
TATGTACACTGCTTTCACTTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
TTTTATTAATAAAATGCTTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQLETA
LEHKEQFHYFILINCANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTTVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNFDSLVIELKAEDRSKFL
DALISLLS

100211-225560

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

100241-656860

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTCTAGTGAAC
 CACGAAGGGGACGATACCGAGAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATT
 GAGTAAAGTAGCTTCCGCTCACC**ATGGT**GACAGCCCGCTGGGTCCCGCTGGGACGCGCTC
 CTGCTCTTTCTCCTGATGTGTGAGATCCGATGTGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG
 CCTCTTCTCCGGCCCGCCCCACGCCCTGCCTGAGATCAGACCCCTACATTAATATCACCATC
 CTGAAGGGTGACAAGGGGACCCAGGCCCAATGGCCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCCGCAAGACGGCCCTGCACAGC
 GGCAGGACTTCCAGACGCTGCTCTTCGAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGGCACCGCCAGTTTGTCTGCCCTGCGTGGCATCTACTCTTCCAGCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACGAGAAAGAGGCTGTCATC
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACTTCCAGCGCCACCTCATCAAGGCCAGGAGACG**AGTGA**AGG
 CCTCTGGGCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTGTGACTGCTGTGAAGCAGGAAGGCCAGGGAGTCCCGGGGACCTGGCATCTGGGGAGA
 CCGTGCTTCTATCTTGGCTGCCATCATCCCTCCAGGCTATTTCTGCTCTCTCTTCTCTCT
 TGGAGCTATTTTAAAGAGCTTGTAACTTAAATATCTAGAATTTCCGAGCTCCGTAGGCC
 AGCACTTCTCAAATCTGGAATGCAATGCAGAAATCACCCGGGGTTCGTGTTAAATGCAGATTCT
 GACTACAGCTCTGAGTGGGTCCAGGATTCTGTGTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACTGGAGCAACAGGTTCTTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTTGGAATCCTCCACATTTAGAAATCTCCCAACTTTTTTTTCT
 TGAGACAGAGTCTTGTCTGTTGCCAGGCTAGAGTGCAGTGGTCCAACTCTCAGTTCACTGC
 AACCTCTGCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCATAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTGGCTAATTTTTGTATTTTATAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGTCTTGAATCCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCTGGCCAATTCGAACATTTCTAAATTTCTCTCAT
 CCGTCCAGGGCTCCCGTGCTATGTTCTCTTTACCCCTTCCCGCTTCTCTTGTCTCAGGCC
 TGCACCACTGCAGCCACCGTTCAATTTATTCATTTCATTAAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTCAACACAGGCCCTGCCCTGCCCTCAGTGACTGGCCA
 GTCCAGCCAGGCCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCAGAGCTATGGGG
 GCCTGTGTTCTGGGTGTTACAGTCTGCTGGTCTCCTATACCACTGCTCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGAGGTATCTCCTTCCCGTTCTCTATCCACCTGCCAG
 TGCTCATCGTTACAGCAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGGTGTGGGGGATTTGGGGGGTGAAGTGGCCCCCGAAGAAATGGAACCCACACCA
 TAGCTCTCCCTACAGCTGATACGGCATCTCGCAGAAAGACCTGCCCTCCTCACTGGGATCCC
 CTTCCTGCCCTCTCCAGGGCTCTGCCAGGGCCCTTGCTCAGTCCCTTCCACCAAGTTCATCT
 GAACTTCCGTTTCCCGAGGGCTCCAGTCCCTCAGCACTGATGCTGTGCTCCCGAGGTGCT
 CTCTGCCCTTCATGCCCTCTCACCAGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGGTGGGCAGCTCTCGTCTCAGAGGCTCTCCCGCTGGTGTGCTGCTCTTAC
 AAACACTGCAGGAGAAGGGGCCAGGAAGCCCGAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAGAGGAGCCCTCAGGCCCTTCGTTTCTTCTTCCAGGGTGGGGTGGCTGGT
 GTTCCCTAGCCTTCCAACCCAGGTGGCTGCCCTTCTCCCGAGAGGAGGGGGCTCCGC
 CCATTTGGTGTCTATGCAGACTCTGGGGTGAAGTGGCCCCGGGGGTGATCTCTGGTGTCTAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGGTCTGACCAAGTGGCAGGA
 AGACCTGGCTATAAACCCCTGCCTGATCTGCTGCCCTGCCGTACCCGCGCACGCCCTGCC
 GTCCAGCATGATTAAGAAATGCTGTCTCCTCTTGGAAAAAAAAAAAAAAAAA

00000000 10000000 10000000

FIGURE 30

MVTAALGPFVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDGDPGFMGLPGYMGREGFPQGEFPGQSGKDGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCACCCGCCAGGAAAGACTG
 AGGCCCGCGCCTGCCCGCGCCGGCTCCCTGCGCGCCGCGCGCTCCCGGGACAGAA**GATG**TG
 CTCACGGGTCCCTCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGGCCACAGACAGTCTTCTGCAGCTGCCCGCCAGGGG
 ACCACGGTGCCCCAGACGTGCCACCCGACACGGTGGGGCTGTACGCTCTTTGAGAACGGCAT
 CACCATGCTCGAGCCAGGCAGCTTTGCCGGCCTGCCGGGCTGACAGCTCCTGGACCTGTCAC
 AGAACAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAACAGGTGCATGAAATCACCATGAGACCTTCCGTGGCCTGCGCGCCCT
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACTCCAGCAGCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCACACTGTGATCCGAGGCCTCCGGGGCTGACGCGCTCGGGCTGCCCGCGCAACAC
 CCGCATTCGCCAGCTGCGGCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCGCGCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCCCTG
 GGTGCGCAGAGCCACGTCACTGCGCAGCCCTGAGGAGAGCGCGTGCACCTTCCCGGCCA
 AGAACGCTGGCCGGTCTGCTCCTGGAGCTTGACTACGCGGACTTTGGCTGCCAGGCCACACC
 ACCACAGCCACCCACACACGAGGCCGCTGTGCGGGAGGCCACAGCCTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCCTCCA
 CTGCCCCACGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCGGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCGCTGCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCTGATAAGCGGCTGGTGACGCTGCGACTGCCCTGCGCTCGCTG
 AGTACACGGTCACCAAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGG
 CCGGGCGGGTGCCGAGGGGCGAGGAGGCTGCGGGGAGGCCATACACCCACGCCGTCCA
 CTCGAACACCGCCAGCTACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCG
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGCGG
 GGGCGGGCATGGCAGCAGCGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT
 GGAAGCTGAGGGAGTGAAGTCCCTTGGAGCCAGGCCGGAAGGCCACAGAGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGCCTGGCCTC
 CAGTCAACCCCTCCACGCAAAGCCCTACATC**TAA**GCCAGAGAGAGACAGGGCAGCTGGGGCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCGCCCTCCTGCTGCCACACCAAGTAAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGCTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGACGCTCCCTGGGCACGGC
 GCGCCTGCCATGTGCTGGTAACGATGCTGGGTCTGTGCTGGGCTCTCCCATCCAGGCGGA
 CCTTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGACAGAGGGGACGCGGCTAGGCGCGTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCAATTATCTCG
 GGAAGATGTTTTCAAACCTCAGAGACAGGACTTTGGTTTTTGAAGACAAACGATGATATG
 AAGGGCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAA

MCSRVP LLLPL LLLL LALGPGVQGCPSGCQCSQPQT VCTARQGT TVPRDV PPD TVGLYV FEN
GITMLDAGS FAGL PGLQL LDSLQNQ IASLPSGV FQPLANLS NLDLTANR LHEITNET FRGLR
RLERLYLGKNRIRHIQPGA FDTLDR LLELKLQDNELRALPPLRLP RLLLLDL SHNSLLALEP
GILDTANVEALRIAGLGLQQLDEGLFSRLRN LHDLDVSDNQLERVPPVIRGLRGLTRLR LAG
NTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRL LAAARNPFNCVCLPSWFG
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVP TTRPVVREPTALS
SSLAPT WLSPTAPATEAPSPSTAPPTVGPVPQPD C PPSTCLNGGTCHLGRHH LACLCE
GTYGLYCESQMGQGT RSPSTPVTPRPPRSLTLGIEPVSPSTLRVGLQRYLQGS SVQLRSLRL
FTNLSGPDKRLVTRLPLASLA EYTVTLQRPNATISV CVMPLGPRGVPEGEEACGEAHTPPA
VHSNHAPVTPQAREGNLPLLIPALAAVLLAALAAVGAAYCVRRGRAAMAAAQDKGVGPAG
PLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFP GPGLOSPLHAKPYI

FIGURE 33

GAATCATCCACGACCTGCAGCTCTGCTGAGAGAGTGAAGCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTATATGAGGAAATAAGTGGTAAAACTCCTTGGAAATACAATGAGACTCATCAG
 AAAACATTTACATATTTGTAGTATTGTTATGACAGCAGAGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGCCAACTGCTCCAAACATGCTCTAAGAAAGGTTCCCCGAGACTTC
 ACCCGGCCACACAGCAGTGGATTTATCCTATAACCTCCCTTTTCAAACCTCCAGATTTCAGA
 TTTTCATTCTGCTCCAACTGAGAGTTTGATTTCTATGCCATAACAGAAATTCACAGCTGG
 ATCTCAAAACCTTTGTAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTTAATAACAGACTC
 AAGAGTTAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTCTTTTAAATGACTTT
 TGACCCATGGCTATCTGTGAGGAAGCTGGCAACATGTCACCTGGAAATCCTAGTTGTTGA
 TGGGGGCAAAAATCAAAAATCAGATTTCCAGAAAATTCCTCATCTGCATCTAAATCTGTCT
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGGTAGCTGCCCTATCTAAACCAAC
 AAAACTGCATTTGTTTTACCAATGGACAAAATTTCTGGGTTCTTTGGCTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCAAATTTGTAAGTTATGA
 ATGCAACGAAATCTTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACTC
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTCTGACTAC
 TCAAAATCTGTAATGAGAACTATAAAAATGGAGCATGTACATTTACAGAGTGTTTTACATTCA
 ACAGGATAAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAAATG
 CACAAATGGCCACACATGCTTTTCCCGAATTAATCTACGAAATTCATTAATTTAAATTTTGGC
 AATAAATATCTTAAACAGAGAGTTGTTTAAAAGAACTATCCAATCGCTCACTTGAACAACTC
 CATTTTGAATGGCAATAAATCGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACACACAC
 CCTTGGAACTCTGGATCTGAGTCAAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGGCCAGAACTGTGGTCAATGAATCTGTCAACAATAAATTTGCTGATCTGTCTTCAG
 GTGCTTGCCCAAAAGTATTCAAAATCTTGACCTAAATAAATCAACCAATCAAACTGTACCTTA
 AAGAGACTATTTCACTGATGGCTTTACGAGAGACTAAATATTGCAATTTAATTTTCAACTGAT
 CTCTCTGGATGCATGCTTTTCTAGTAGACTTTCAAGTTCTGAACATTGAAATGAACCTTCTTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATGCGGGAAGAA
 ATCCATTCGGGTGATGCTGTGAATTAATAAATTTTCACTCAGCTTGAACATATTTCAAGGTC
 ATGATGGTTGGATAGCTCAGATTATACACCTGTGAATACCCCTTAAACCTAAGGGGAACATG
 GTTAAAGACGTTTATCTCCACGAATTTATCTTGAACACAGCTCTGTTGATTTGCACCATTTG
 TGGTTATTATGCTAGTTCTGGGTTGGCTGTGGCTTCTGCTGTCTTCACTTTGATCTGGCC
 TCGTATCTCAGGATGCTAGGTCAATGCACAAACATGGCAGAGGTTAGGAAAAACAACCCA
 AGAACCACTCAAGAGAAATGTCGGATTCACGCATTTATTTACACAGTGAACATGATTTCTC
 TGTGGTGAAGAATGAATTTGATCCCAATCTAGAGAAGGAAGATGGTTCTATCTGTTATGTC
 CTTTATGAAAGCTACTTTGACCTTGCACAAAGCATTAGTGAAGAATATTGAAGCTTATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTTCCAGAAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGCCACCAACATCTCTTCCATGAAAATTCGTGATCATATAATTTCTATC
 TTAATGGAACCCATTCCATTTCTATTGCATTTCCACAGGATCATATAAATGAAAGCTCTCTCT
 GGAAAAAAGGCATACCTTGAATGGCCCAAGGATAGGCTAATGTGGGCTTTTCTGGGCAA
 ACCTTCGAGCTGCTATTAATGTTAATGATTAGCCACCAGAGAAATGTATGAATCGCAGACA
 TTCACAGATTTAATGAGCAATCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTTGCT
 ATAAAATCCACAGCTCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGACATAATTTATAAATAAAAAATGGTTATTCTCCCTCATATA
 TCAAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTCAACAGTTTATAAGG
 GCTTATGAAAAGAGGTGTTCTCCAGGATGTTTATAATGATGAAAATGTGGCCAGGTGCG
 AGTGGCTCACTCTTGTAAATCCAGCACTATGGGAGGCAAGGTGGGTGAGCCACAGAGTCAA
 GAGATGAGAGACCATCTTGGCCAACATGGTGAACCCCTGCTCTACTAGAAAATACAAAATTA
 GCTGGGCGTATGTTGCCAGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGACAGGAGAAATCG
 CTTGAACCCGGGAGGTGGCAATTTGCAGTGCAGCTGAGACTGACGCCATGCATCCAGCTGGT
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAATCAATCC
 TCAATGGCCACAAAATAAGGCTAATTTCAATAAATATAGTACATTAATTAATAATATA
 CATGCCCACTAAAAAGATAAGGTAGCTGTATATTTCTCGGTATGAAAAAACAATATAATAT
 GTTATAAATATAGGTTGGTGCAAACTAATTTGTGGTTTTTGGCATTGAAATGGCATTGAA
 ATAAAAGTGAAGAATACTATACCAGATGTAGTAAACAGTGGTTGGGTCTGGGAGGTTGGA
 TTACAGGAGCATTTGATTTCTATGTTGTGTATTCTATAATTTGTTGAATGTTTAGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTCACGCT

00999999 "11004 1002115228866

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHVSVKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMShLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLELILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILtDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENCsWPETVVNMNLSYNKLS
DSVFRCLPKSIQILDlnnnqIQTVPKETIHLMALRELNIAFNFLTDLPgCSHfSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFrCTCELKNFIQLEtYSEVMVgWSDSYtCEYPLN
LRGTRLKDVHLHELSCNTALLIVtIVVIMLVGLAVAFcCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYfDPGKSISENI
VSfIEKSYKSiFVLSPNFVQNEWCHYEFYFAHhNLFHENSdHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKGLFWANLRAAINVNVLATREMYELQTfTELNEESRGSTISLM
RTDCL

[illegible]

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNKSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNP DGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSYST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR
LKLGRGRRRQRG

FIGURE 38

MRPGLSFLALLFFLGQAAGDLGDBGPIPSPGFSSFPBGVDSSSSSFSSSSSRSGSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMVYNYNTGNIARVNLTNTIAVTQTLPNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGLVYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDDQKLYVYNDG
YLLNYDLSVLQKPQ

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GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAGATCAAACACCCCTGTCGTCAC
CCTCTCCCACTCCAGGGAGCTGTGCTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCCACTGGATGATTGCTTATTGTATATAAATGCTCGAGAGTT
CGGGATCACCATTGGCCAGGTAGTGGTACAGCGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGGTTAACTTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAGATGGGGGAGCGCTCTGGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTGTGTGGAAGTGCCTCGTGTGTGCTATGCCGATGCTGTCTGTGGAAAC
 AACTCCCACTGTAACTAGATTGATCTATGCACCTTTTCTTGCTTTGGAGATGTGTACCTGT
 TGTAAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCCTGGATTCTGTGAGAATG
 AGAAAGAGTGTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTCTGTTT
 GGTTTGGCTATGTTCTATCTTCTCTCTTTACTAATGTCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTCTTTAAATTTGCTGCGACAATTCGAATTA
 TTATTGGGGCATTCTTCATTTCCAGAAGGAACCTTTACAACTGTGTGGTTTTATCTAGGCATG
 GCAGGTGCTTTTGTTCATCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCGAGCTTGT
 TATCAGCTACAGCTCTGAATTAATCTGCTGTCTTTAGTTGCTATGTCCTGCTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTCCAGAAAAAAGGCGTTCATCAGTGTCAACATGCTCTCTG
 CGTTGGTGTCTCTGTAATGTCTATACCTGCCAAAAATCCAAGAAATCAACAACAGATCTGGTT
 TGTTCAGTCTTCAGTAATTAACAGTCTACACAATGTATTGACATGGTCAGCTATGACCAAT
 GAACCAGAAAAAATTCGAACCCAAGTCTACTAAGCATAAATTTGGCTACAATACAACAAGCAC
 TGTCCCAAAGGAAGGGCAGTCACTCCAGTGGTGGCATGCTCAAGGAATTTATAGGACTAATTC
 TCTTTTGTGTGTGTATTTTATTCAGCATCCGCTACTTCAAACAATAGTCAGGTGATAAAT
 CTGACTCTAACAAGTGTATGAATCTACATTAATAGAAGATGGTGGAGCTGAAGATGATGAATC
 ACTGGAGGATGGGAGCGATGTTCAACGAGCTGTAGATAATGAAAGGAGTGGTGTCACTTACA
 GTTATTCTCTTCTTCTTCTTCTATGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC
 AACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAAGTCACTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATGCTGCTGTATGTTTGGACACTCGTGGCACCCTTGTTC
 TTAACAATCGTGATTGTGACCTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTAATTGC
 TTATTGAAAAACAGTATTCCCACTTTTGTAAAGTTGGTATGTTTTTGTCTCCCATGTAAC
 TTTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAA
 GTGCATTGATGTGAAGTAGAATGAATTTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT
 TAGTAAAGTGGCCATTATTGGGCTTATTCTGCTCTATAGTTTGTGAATGAAGAGTAAAA
 ACAAAATTTGTTGACTATTTTAAAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATTTAA
 GCAAATGTATGGCTGCCCTTTTGAATATTTGATGTGTTGCCCTGGCAGGATACCTGCAAGAAC
 ATGGTTTTATTTTAAAAATTTATAAACAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGATGG
 TTATGGATGGAGGTGTGCGTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAAGTGTGTTGGTTGTTTTAACTCATGAAGTATGGGTTCACT
 GGAAATGTTTGAAGTCTGAAGGATTTAGACAAGGTTTTGAAAGGATAATCATGGTTAGA
 AGGAAGTGTGTTTTGAAGTCACTTTGAAAGTTAGTTTGGGCCCAGCACGGTAGCTCACCCCTT
 GGTAATCCCAGCACTTTGGAGCTTAAAGTGGGTAGATTACTTGGAGCCAGGAATTCAGACCA
 GCTTGGCAGATGGTGAACCTGTCTATAAAAAATTAATCTGGCTTTGAGCATATGCTGTGGTCT
 CAGCATGTAGAGGCTAGTGAAGATTGCTGAGCCAGGCAAGGTTGCACTGAGTGAAGTCA
 CGTCACTGCACCTCTAGCTGGCAGAGTAAAGCAAAAAATATATATATTGAAATCAAGG
 AGGCAAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCCTTAGGCTTTAGTAGGCTACTTAT
 ATAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATTA
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATTAATGACATTCTCTCGACATTTAA
 AAATAATTTCTATTCAAATACATGATATTTGATTACACCTCATACTGTGTAATTAATGT
 GATGTGATTGCTGGTCCAGCATGCCATAAACCAAGTGAAGAAATGAGTGAATGTTT
 AGAATAAATCCTGCTTATAGTATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATGGAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT
 ATTGAGTTTGTATTTTGTATGTGTCAGTGTCTAATGAAGCTTTTAAATCTTCAAAAT
 CTTCTGTTTAAAAATTTTAAATGTGAATGGAATATAACATTCAGCTTAAATCCCCAAC
 TTATTCGTGTGTAGACATTGTATCCACAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAAATAAAAAA

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MGVSLGLCSMASWIPCLCGSAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNINLVGYKAVYRLCFLGAMFYLLSLMLIKVKSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFVVGMAGAFCEILIQVLVIDFAHSWNESWVEKM
EEGNSRCWYAALSLATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTVYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGI
VLYVWTLTAPVLTNRHFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

123456789101112131415161718192021222324252627282930313233343536373839404142

GTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGCGCAGCTGGATAAC
CANGTTTGTGTGGAAGTGCCCCGTGTTGNTATGCCGATGCTGTCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGTGGAGTANGTGATAGCTTGTGTAAT
GTTGATACCAGGAATGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCGAGTGCACAATGGATTTTGGTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

AAGAAGCTGTCTCCAICTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
 GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGAAGTGCCCCGTGTT
 TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCACTGTAAC TAGATTGATCTATGCACATT
 TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAACAACCT
 GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATTTTGGTTG
 GCTATAAAGCTGTATATCGTTTGTGCTTGTGGTTTGGCATGTGTTCTATCTTCTCTCTTTTA
 CTAATGATCAAGTAGAAGATGACGTAGCTATGACGTGTCAGTGTCAGTGCAACATGGATTTGGTT
 CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

GCTGTCCCTTAGTGGAAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCTCTG
 CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
 AGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGCCCCCTGTGAACATTTTGGTTGGC
 TATAAAGCTGTATATCGTTTGTGCTTTGGTTGGCTATGTTCTATCTTCTCTCTTTACT
 AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
 TTAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATCTTCATTCAGAAAGGAACTTT
 ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTTCATCCTCATACAACAGT
 CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
 ACTCGAGATGTGGTATGACAGCCTTGTATTACAGCTACAGCTCATGTAATTCTGCTGCTTTA
 GTTGCTATCGTCTGTTCTTTGTCTACTACAGCTACAGCCAGCTGTTTCAGAAAACAAGGC
 GTTCATCAGTGCTCAACATGCTCCTCTGCCTTGGTGCTCTCTGTAATG

[illegible]

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSIITGKYVHNHNTYTNNENCSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLN EYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWMRYTGPMPKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPIYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY
YGGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
PRNLTKRHWP G A P E D Q D D K D G D F S G T G G L P D Y S A A N P I K V T H R C Y I L E N D T V Q C D L D L Y K S
LQAWKDKHLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNTYWC MRT I N E T H N F L C E F A T G F L E Y F D L N T D P Y Q L M N A V N T L D R D V L N Q L
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEYQRQFQRRKWPEMKRPSSKSLGQLWEGWEG

AACAAAGTTCACTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCAC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCGGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
 ATCACCCTCATCTTGGCCAGCTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACC
 CCCGCCACACCCTCACCACCTCACCACCACACCACCCACCGCCACCATCCCCGCCA
 CGCTCGCTGAGGCTGCTGTCGCCGTGCTGTTGGACAGCAGCTGCCCTTGCCCTCCCATCTG
 TTCCACGAGACAAGTGGACCCCATGTTTCCATGTGAAGGATGCATCTCTGGGGTGAACAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCCAGTGTACTATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
 ACAAGCGTGTCTTGGCAGGCTCAGCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
 ATCAGGCTGCTTCCAGCCCTCTGGCGGGCAGGGCAGTGGGAGAGGCCCTGAGAATGTCTTTT
 GGTTTGGAGAAGCAGTGTGAGGCTGCACAGTCAATCTACGCTGCCTTAGTCCAAGAAAT
 AAAAAACCACTAAGAAGCTTTAAAAAATAAAAAAAAAAAAAA

FIGURE 50

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCGCG
 GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCTACTGAGAGC
 TGCAGCATCTCTCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGGGCAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCCCTCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCCTCTGGGGAGGAGGGGTCTGAGGGACCTGACTTCCCTGTC
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA
 AAAAAAAAAA

CCCGGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCCCTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTGCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTACTGGCTTAAAGCTGGTGAAGGCGCATTTTGCCTCTGGTAG
GGATGGCCATGTGTGCCCACTCTCTGGGCTCATTTGGGTATCAACTATACAGAAAGGCCAAT
AGACCCAAAGTGTCCA AAAAGAAAGCTCAAGGAAGAGAAACGAAACAAAGAGCAAAAAGAAAT**A**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAGAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

0989297-11001

FIGURE 54

CCCGGGAACGTGTTCTTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

00000011001

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTTAAAAAACTTAAAA

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTGTGTTTTCTTGCTAAAAATCGGGGGAG
TGAGGCGGGCCGGCGCGGCGACACCGGGCTCCGAACCACATGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTCAACCACTCATACCATGCCT
GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
TTGGAGGGCTGTTTTTAAGTTTGGCCGCATGAAGACTTATGGCAGTGAACACATCTGAT
TTCCCAACAGCACACAGCCCTGCATGGGTTGTGTTGTTTTTACTGCTCACTCCCAACCTT
TGTGAATGCCATTTTCTAAACTATTCTCGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAAATCTATTGTGGTATGCATTGTTAACTT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
TGTAATAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTGCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTAAATGTGTTTATTCAAATGTGGT
CTCTCTGTGTCAAATGTTAAATGAAATATAACATTTTTAGTTTTTAAATATTCCGTGG
TCAAAATTCTTCCTCACTATAATTGGTATTACTTTTACCAAAAATTCTGTGAACATGTAAT
GTAACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCAT
CAAGGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCATG

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVNSGQVRGDSYSEGCLGQTGARIWLVFGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGCGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACCTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTGAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGCGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGCCCCGGCGCGG
CGNGACACCGGGTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGTGA**TATG**TGGCTTCCGCTGGTGTCTCTGGCTGTGTCTGTCTGTGGCCGTGC
TCTGCAAGATTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAAGC
TTTTTCAGCCZACCAAGTGCCGAGAAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCTGGCTGCAGTGCAAATCTAGCTAAAGCTGGCAAGCGACTCTGGTGTCTGGACACACAT
ACCAAGGACAGGGGGCTGCTGTCAATCTTTGGAAAGAAATGGCTTGAATTTGACACAGGAAT
CCATTACATCTATTGGAAGAGGCGAGCATTTGGCCGTTTATCTTGGACCATCTGGAAAGGCC
AAGGGCAGCTGGACTGGCTCCCTGTCTCTCTCTTTGCATCATGGTACTGGAAAGGCC
AATGGCCCAAAGAGTACCCATGTACAGTGGAGAGAAAGCTACATTCAGGGGCTCAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAACTATATAAAGCTGTTAAGGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTGAAATTCCTCCATTGCGCGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCATTCCTTCAGCAGCTCCACCCAGAGCTGGCTGA
GGTCTGCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGTACATCTTCCCA
CTTACGGTGTCAACCCCAACCAAGTGCCTTTCCATGCAGCCCTGCTGGTCAACCACTAC
ATGAAAGGAGCTTTTATCCCCAGGGGGTCCAGTGAATTCCTCCACACCATCCTGT
GATTTCAGCGGCTGGGGGCGCTGTCTCACAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCTGTGTGTGTGCTAGTGTGAAGAGGGCAGTGAAGTGAACATCTATTGC
CCCATCGTGTCTCCAACAGGACTGTTCAACACCTATGAACACCTACTGCGGGGAGCGC
CGCTGCTGCGAGGTGTGAAGCAGCAACTGGGGAGCGGTGCGGCCCGCTTAGCAATGACCT
CTGTTTTCATCTGCCGCGAGGCACCAAGGAAGAGCTGCATCTGCCGTCCACCAACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGCTCTCAATGCCAGGGAAGA
GGTGGCGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAAAGAGTCCGACCTGGG
AGGACCATCTCCAGGCGGTCACCATGATCATGCTCATACCCACTCGCTACGAGTGGTTT
GAGGAGTGGCAGCGGAGCTGAAGGAAAGCGGGCAGTGACTATGAGACCTTCAAAGACT
CTTTGTGAAGCCTCATGTAGTGGTCTGAACTGTTCCACAGCTGAGGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCACTCACCACCACTTCTATCTGGCTGTCTCCCGAGGTGCC
TGCTGAGGGGTGACCATGACCTGGGGCGGCTGCACCTGTGTGATGGCTCCTTGAGGGC
CCAGAGCCCCATCCCCAAGCTCTATCTGACAGGCAGGATATCTTCACTGTGGACTGGTCCG
GGGCCCTGCAAGGTGCCCTGTGTGTCAGCAGCGCCATCCTGAAGCGGAACCTTGTACTCAGC
CTTAAGAATCTTGATTCTAGGATCCGGGCAAGAAAGAAAGAAAT**TAGT**TTCCATCAGGGAG
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCATAATGTCTTTCTG
CATTAGTTCCTTGCAGCTATAAAGCACTCTAATTTGGTTCTGATGCTTGAAGAGAGGCCATG
TTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTAGCCCTTTTATAACATGCCATCCCTACTAATAGGATATGACTTGGATAGCTTGTATG
TCTCATGACGAGCGGGCTCTGCATCCCTCACCATGCTCCTCACTGATGATCAAAAGCGA
ATATTTCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTGACTCAACCTGGTGGGTTCAGTTC
TGTCTTGAGGCTTCTGCTCTCATTCATTAGTGTACGCTGCACAGTTCTACACTGTCAAGG
GAAAGAGGAGCTAATAGGCTTAACTCAAACCTGGGCGTGGTTTGGTTGCCATCCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTTCAGTGGCTTTCAGGGGACAGGAAT
GCCTGTGTCTGGCCAGTGTGGTCTTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGATGTGTCAGATGATCATATCCAATTATATGGAAGTCCGGGTCTGTCTTCTTATCA
TCGGGTGGGCACTGGTTCTCAATGTGCCAGCAGGAGCTCAGTACTGAGCCCTCAATCAAGC
CTTATCCACCAAAATACACAGGGAAGGATGATGAGGGAAGGAGTGCATCAGGAGTCAGGGCA
TGGAGCTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGCAATTCCAGCCAAGGG
CAGCAGAGGACAGTGCAGGAGGTGTGGGTTAAGGAGGAAGTGCATCAGACAGAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCAATTTGCAGTTAATTAGCACATGTGAGG
TTAGACAGTGGTGAATGCAAGCTCAAGTTTGGAAAAATCACTTTTCACTTATGTTCTTGG
GTATCAGACATACGAAAGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

FIGURE 64

MWLPLVLLLLAVLLLLAVLCKVYLGFLSGSSPNPFSEDVKRPPAPLVTDKARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIIYCPVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYYVYDMDQAMERYVSMFREEAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTGLVGALQGALLCSSAILKRNLSDLNLDNRIRARQKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACC GGCCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGGTGGCTGCTGAGCTTTGGCCCTCGGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTTCCAAGACTACTTTTGACATCAGATGAGTCAGTAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTCAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAAATCCAGAAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGCTTTTGTGAAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAGGCTCTTGTAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTT
 TCAGCTTTCATGATCCAGATTTGCTTGATTAAAGACCAATATTCAGTTGAACCTCCTTCAA
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTTAAATGATAGTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAAGATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTCTTTTGCTAATTTGGAAGATTAACTCATTTTAAATAAA
 ATTATGTCTAAGATTAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWFCEEEEEAKRRQMGEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGACAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**CATG**GCCTGCCGGTGCCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGGGATTACTACTGCTCTGTTGGC
TACGECTTTAGTCCC**TAG**GGGTGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTTCT
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 69

GCGGCCCGCCCGGAGACCGGGCCCGGGGGCGCGGGCGGCGGGATGCGGCCCGCGGGGCGG
 CGATGACCGCGGAGCGACGCCGCGGGCCCGGCCCTGACCCCGCGCCCGCGCTGTAGCCCC
 CCGCGCGAGCTCGGACAGGCCGAGATGACGCCGAGCCCTGTTGCTGCTCTCTGCTCGCCG
 CGCTGCTGCTGGGGGCTTCCCACCGGCCGCGCGCCCGGAGGCCCCCAAGATGGCGGAC
 AAGGTGGTCCCAACGGCAGGTGGCCCGCTGGGCCGCACTGTGCGGCTGCACTGCCAGTGGGA
 GGGGACCCCGCGCGCTGACCATTGTGGACCAAGGATGCCCGCACCATTCCACAGCGGCTGGA
 GCGGCTTCCGCGTGTGCGCCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCGGCG
 GTGTACGTGTGCAAGGCCCAACCGGCTTGGCAGCCTGAGCGTCAACTCAACCCCTCGTCTGT
 GCTGGATGACATTAGCCACAGGAAGGAGAGCCTGGGGCCCGCAGACTCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGGCTTACACAGCCCTCCAAGATGAGGCGCG
 CGGGTGATCGCACGGCCGCTGGGTAGCTCCGTGCGGCTCAAGTGGCGGCCAGCGGGCACCC
 TCGCCCCGACATCAGCTGGATGAAGGACGACCGGCTTGAACGCGCCAGAGGCGCGCTGAGC
 CCAGGAAGAAGAAGTGGCACTGAGCCTGAAGAACCCTGCGGCCGGAGGACAGCGGCAAAATAC
 ACCTGCGCGCTGTGCAACCGCGCGGGCGCCATCAAGCCACCTTACAAGGTGGATGTATCCA
 GCGGACCCGTTCCAAGCCGCTGCTCACAGGACGACCCCGTGAACACGACGCTGGACTTCG
 GGGGGACCAAGTCCCTTCAAGTGAAGGTGGCGAGCGACGTGAAGCCGGTGATCCAGTGGCTG
 AAGCCGCTGGAGTACGGCGCCGAGGGCCGCAACAACCTCCACATCATGTGGGCGGCCAGAA
 GTTGTGGTGTGCTGCCACCGGGTGACGTGTGGTGGCGGCCGAGCGCTCTCACTCAATAAGC
 TGCTCATACCCTGCGCCGCGAGGACGATGCGGGCATGTACATCTGCTTGGCGCCAAACACC
 ATGGGCTACAGCTTCCGACGCGCTTCTCTACCGTGTGCGGACGCAAAACCGCCAGGGCC
 TGTGTGGCTCTCTGCTCTCGGCCACTAGCTCGGCTGCGTACCGCTGGTCTATCGGATCCAG
 CCGCGCTGTCTATCTCTGGGACCCCTGCTCCTGTGGCTTTGCCAGGCCAGAGAAGAGCCG
 TGACCCCGCCGCTGCTCCTCTGCTGGGACCGCCGCGGGGACCGCCGCGGACCG
 CGCGGAGACAAAGGACCTTCCCTGCTGGCGCCCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTAGGACGATGGGTCTCGGCGAGCCCGGACACTTACTGGGCGCCAGGCCAGTGTCTGGC
 CTTAAGTTGTACCCCAAACTCTACACAGACATCCACACACACACACACACTCTCACAC
 ACATCACACGTGGAGGGCAAGGTCCACAGCACATCCACTATCATAGTGTCTAGACGGCACCGT
 ATCTGCAGTGGGCACGGGGGGGGCGCGCAGACAGGCGAGCTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGACGGGGACCATGGCGAGGAGGAATGGCGAGCACCCGAGGCGAGTCTGTGTG
 TGAGGCATAGCCCTGGACACACACACAGACACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACAGCTGCTCCTGAAGGCACACGTACGCACACGACATGCGCAGATATG
 CCGCTGGGACACAGATAAGCTGCCAAATGCACGCACACGCACAGAGCATGCCAGAAAC
 TACAAGGACATGCTGCTGAAACATACACACGACACCCATGCGCAGATGTGTCTGGACATG
 CACACACACACACGAGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCCCTTGACACACACATGCACGG
 ATATGCTGCTGGACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACACGTGCACAGGCGCAGATATGCT
 GCTGGGACACACGAGATATGCTGTCTAGTCACACACACGACAGACATGCTGTCCGGACAC
 ACACGCGATGCACAGATATGCTGTCCGGACACACACGACGACGACAGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCTCAACACTCACACACGTCAGATATTGCTTGGACACACACA
 TGTGCACAGATATGCTGTCTGGACATGCACACACGTCAGATATGCTGTCCGGATACACAGC
 CACGCACACATGCAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACACAGGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCTCAACACTCACACACGTCAGATA
 TATTGCTTGGACACACATATGCTGCTGCACAGATATGCTGTCTGGACATGCACACACGTCAGATA
 TGCTGTCCGGATACACACGACGACACATGCAGATATGCTGCTGGGACACACTTCCGGAC
 CACACATGCACACAGGTGCAGATATGCTGCTGGACACGACAGCTGACGCTGCTTTGG
 GAGGTGTGCGCTGAAGCCTGACGTACGTGTGCGGTGAGGCTCATAGTTGATGAGGACTTT
 CCGTCTCCACCGTCACTCCCCAACTCTGCCCGCTCTGTCCCCCGCTCAGTCCCCCGCTC
 CATCCCCCTACTGCTGTGGGCTGGGGTTGGGGGACAGCAGCCCAAGCCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCCAGTGCAATTTCCCCCTGACACAGAGAAGGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTCACAGGAC
 TGTGTTCTCTCTGGGGCCCGGGGACCCGCTGCTTTTACGCACTGCTGATGACCAACCCCG
 GTCAGGCGCAGACACCACCCCCACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAAATTTTA
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTATTTTGTAAACACAAA

FIGURE 70

MTSPLLLLLLPLLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPLTM
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSAPAQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHTSHVEGKV
HQHIHYQC

[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ
 RPGQNCNYYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDSGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCATGKPRPDYFVYHNDTLLDPSLYKHESKLVLRKLQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPEYLRIRLPHDCFQATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCKGISTEEREIQCSGYTLPTKVAKECSCQRCETETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPTITLEAMETNIIPLGEVVGEDPMAELEIPRSFYRQNGEPYIGKV
 KASVTFLDPNISTATAAQTDLNFINDGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHEDPR
 VKKTAQISMAKPRPNASAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVIIPQGSCRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMPLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSBGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

MYLSRSLSIHALWVTSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDL SQHTVLEI ICTEESTGYTTNSKI IHFEIKDRFALFAGPLRLNMA SLYGQLD
TTKKLRDFFTVDLRI RLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKN LHATVCYVDN
SKLTCECEHNTTGPDCGCKKNYQGRPWSPGSYLP PKGTANTCIPSISSIGTNVCDNELH
CNGGTCCHNVRLCPAAYTGILCEKLRCEEAGSCGSDSGQAPPHGTPALLLLTLLGTAS
ELVF

FIGURE 76

MSVIFFACVVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCTCGGAGACCTGTGGTGGGAATTCACAGCTTCNTATGACACTACTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATT
 TTAACATGTAAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAAATGGGGT

FIGURE 79

MEAPDYEVLSVREQLPHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIISNEVLSLSPRNYIYQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFTESEGFGAGSRKGVLRVYETVVMMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISIFLGVLLLLVCTPLGLARMSFVTGKLLVKPRILLEDLEEQYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKKRKASAWQRNLGYPLAMLCLLVLT
GLSVLVAIAIHLELLIDEAAMPGRMGCTSLGQVSFSKLSFGAVIQVVLIFYLWMSVVVGFY
SPLFRSLRPWHDMTAMTQIGNCVQLLSSALPVFSRTLGLTRFLLDGRFNNWLNIFY
IVFLYNAAPAGLTTLCLVKFTAAYRAELIRAFGLDRPLPVSGFPQASRKTOTOHO

GGCTGCCGAGGGAAGGCCCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTCCCCGGGGCCACAGAGGACCTTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCACAGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGACCCGCTTC
AAGAAGCTGCTGAGTTCACACAGCTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCCTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCCTAGGCTGGGTCTGGTGCCTTGGCGGCGGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCCTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCAAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGAATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCCGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

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[illegible]

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDIFSHFFGDFGMFGGTFRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFIDGEGEPHVDGEPDGLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGKHVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTGTAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCTGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCNTGAAGTGCCTTNTATAAAGGATATTAATAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCGTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAAGATGGTNATCAGAGCTCCCATGGAGACATT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

GGACACGAGGCGCGGGCAGTCGCGGGATGCGCCCGGAGGCCACAGCCTGAGGCCCTCAGGT
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCTCTTCCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGAGCC
TTGGTGCTGGTTTGACGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATT
TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCGTTATACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGCCAAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCTCCGTTGGACCCCAAATCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
AGTCTCTGTGCGGTGCTGAGGAGCATTGTGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCTGTCAGGAGCAGTCTGCAATTT**TAG**GCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTACGCTGTGTGTCATAG
TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAAGTTGCAAACTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTGACGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTCACATTAAATAGAAATTTCTGGCTCTCTCGATCGGTGAGAAATG
TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAGTATGAGGGTTTC
TTCTTTTGGAAGACTTGTACTCTCTCACCTGGCTGAGTTTCATTTATTGATTATCTGCGCT
GGTCCCTGAGCGCTCTGGGTCTCTCCTCTCCCTTCAGGTTGTGGTTTGAAGCTGAGGAAC
ACAAAGTTGATGATTCTTTTATCTTTATGCTTCGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCTCAAAAAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSA
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTGGAGTGTTTTCTCTGTTCTTTGGAATGATTCTCTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAGAACATTAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTTCTAG
 GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TAA**CAACA
 AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCCTGTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGCTCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTCTCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGTGTCCCCACCACTGCAGCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCT
GGCTTTTGAATTGGTTTAGAAGAACATTAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTGGGGTGTGATTTGATGTCCTATTGGTTGGCCTTTGATAGGCATG
ATCTCGAAATTTATGGAATTTTTCTCTGTTC

GGCACGAGGCTGAACCCAGCCGGCTCCATCTAGCTTCTGGTTTCTAAGTCCATGTGCCAAAT
GGCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTTGATCTTTCTTCTCTGGAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTACGTCCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
GGGGCACGGAATGCACCATCTTACCGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTCCT
GATTCACTGTGAGGCGACAGGTTTCAGGAGAAGAACGATGATCAGCATGCAGGTGGCGCC
GGGCTCAAGGGGCTGCCCTCGCTCAAGCATCACTTGTGGCCAGAACAGGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTACGCTGTATATGACTGTACACTCAATTCAGAAA
TAATGAAATCCAACACTGCTGGGAGTCTTAAACGGAAGAAATACCATGCAGATTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGA
GACGCCATGGTGCCCCCGCGCGCCCTGGACCTCGTGAAGTGGCTGTTTGGGCTCGC
TGGTGCTCTACCTTTTCTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACT
GACTCAGGGAGGTGTCAACATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGACCAAGGGGACAAGTCCCGTCTTCACTGTTTGGTGCTGAGTTTTCTGT
AACCCTTGTTGCCAGAGATAAAGTGAAGAAAGTCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAATAAATGAAGTGGCTTTTCTGGGTCAAAAAAATAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTHLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGGSKVLAKE
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFATVRSLRNVVSAYVDCTLNFRNNENPTLLGVINGKK
YHADLYVRRIPLEDIPEDDDDECSAWLHKLYQEKDAFQEEYYRTGTFFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSITLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

[illegible]

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDDDRWFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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10001-10000

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVS VVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWN NFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNQD NSVQVSQKVFQGC GPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSR YLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCACTTACAGCTGCACCGACAGTTGCGAATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTG
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGCCAGAAGTGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCTAGCAGTGTCTGGGCTGCCAAGAAAGC
AGTGCCCCCTGTGATCATTTCAGGGCAATGTGAAGAAAAAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTGAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTTCTTCTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGTGCTCT
TCTAGTGCTCTTCTCTCTCGTAGCTCTAGCCTGTGCGCTCCCTTCACTAGGCTTAGGCTT
AATTACTGTAAAGATTCCAGGAAACTGTAGCTTCTGAGTCTGCTTACCTTAACCTTAATATG
AATCAGGAAAGTAGCAACAGAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KEMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTTAGAAAGTTAGAATAAATATGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRLTVVLGLLVLFLTCYADDKPDKPDDKPDDSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

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GGATCGCCAGCGCCTGCAGAGGCTGAGCAGGGA AAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCC **ATG**GACATCCTGGTCCACTCCTGCAGCTGCTGGTGCTGCTTCTTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
CCTACTGTATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCTTGACAAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACCTCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTCTGCAGGAGGTCC
GGAGACTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCTTCTATGTGCGCAGCAAGTTTTCTGAGCCCACTGGAAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAAGTTCTCCGAAATCCAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCTTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCT **TAG**CAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTGACAGATGAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTTTAATAAATAGACGA
AACCAGC

FIGURE 103

MDILVPLLQLLVLLLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEYPYGSWAFM
WQQVFEPYTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLVPVGPVHIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYLPRLGT

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GTGGATTATTATTGAGTGAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGC
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAGTAACATCATCATCTTGG
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCTCAGCTTGAGCAGTTTG
TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCTCAACCTATAGACTTTGTCCAA
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACGACAACACTCGCTCCAAT
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAAGGAA
AAGTAAGAGGAGTCTTGACCGAGGGGAATCCATGAAACCTTTAACTTTTGAAGGTTCTAC
TTGCGAATTTCTGGTTCAGCCAGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
AGGTGCAATTCTTGCCCTTTTACAATACAGCAGTGAAGCCAGGACATCGAGCTGCATTTTCAG
AAGATTGTGATTCAGCCTCTACTAAGTTGTGTCATCCGTGGAGCAGGAAACCGACAATTAC
ATTGGCTATCTTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTTCCATGAAAGCCAGCACTTG
CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAACGACAGAATATACTA
ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
GGTAGCATCACAAACCTCTCTGCTTATCGATTTTATCAACAGCACTCTACCATCGATCC
TATGTGGAATGTCGCCACCTTGGTTCAGTGCTGGA AAACGATATTCACCTCAGTTTGTA
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGAAGGACTGCTTCATAT
ACTGATGTTTGGGAAAATGTTATATTCAGACCAACAGGCAAATTCACCTAATCCGAAG
ATATACCGAGATCTCAACATATAAGCTGAACAGAAATTTGAAGCTGTAGCAAGCATTCTCAG
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
GCAAGCCATGGA AAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGTC
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
TAATTCAAAAGTCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAATAAACTT
ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDI LALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTL LAGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAAKLLHWNHGLKFPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCACGCTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCTGCGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGAGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGAAATGTAG
 GGCTCAACCTATAGGACTTTGTCCTCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTATCGCTGCGTCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCATAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCAAGTACAATTACATGGCTATCTTGACTATAAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAATAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCAGT
 GCTGGAACAGATATTACCTCAGTTTGTTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTCCA
 GACCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAATAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTGAGCTAGCTGGTACAGATAAATCAAACTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA

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FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCT**ATG**GGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCTCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTTGAGAAGGCCCCACCACCCAGAAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCT**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCAAGGGCCAAGGGTCAGGGGCCGGTCCACTCTTTCCTTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAA

MGAAISQGALIAIVCNGLVGFLLLLLLWILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPSPLEPRT

GTTTGAATTCCTTCACTATACCCACAGTCCAAAGCAGACTCACTGTGTCCAGGCTACCA
GTTCTCCAAAGCAAGTCATTTCCCTTATTTAACCAGTGTGTCCCTCAAACACCTGAGTGCTA
CTCCCTATTTCATCTGTGTTTGATAAATGATGTTGACACCTCCACCGAATTCCTAAGTGGAA
TCAATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCTCGCATTAGCCTTGTCTTTGGCC
ATGATGTTTACCTTCAGATTATCACCACCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
TTTGGGATGTGTTGTTTGTCTGCGGTGTTTATGTTGGCTGTATTATGACTATACCAACGACC
TCAGCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGTTTGTCTATCGTA
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAATT
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTC
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGTCCCTCTGGTGCTGTGCTGCTG
AGCCTGGGAACTCAGAGAGCTGCCAGGTTATGGAAGGGCCCAAGTGGAAATATAAGCCCT
TTCGGCATTCGTGATGTGCTGCTAGCTTTAAATGGCCCTCATGTGACATAGTGAAATCA
TCCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTATTATTTCAACAGAAGT
AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA
TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTGTCCAGGTACCTGTTCCGA
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
TGTCCAAGAACTCAAGTCACTTACATCTATTAAGTGCCTTGAGAGCTTCATAATTTTTCTA
GGAAGGTTAGTGGTGTGTTTCACTGTTTTTGAGAGGACTCATGGCTTTTAACTACAATCG
GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGGCC
ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGAT
CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
CGTAAAAAGGAGCAACAAATTAACAATGCAAGGACACAGCAGGACAAGCACTCATTAAAGGA
ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTATTAGGTATCTGTACCT
AGAAAAACATTTCTTCTAAGAGCCATTACAGATAGAGATAGAGACCATAGAGAAAAGTT
AGTGAATTTTTTTTTAAAGACCTAATAAACCTTATTCCTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALS LAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGACCTCTCCTGTCTTCCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAGCCTAAGGGGAAAAAGAAATATTCATTCTG
 TGTGGTGAAAATTTTGGAAAAAAATTCCTTCTTCAAACAAGGGTGTCACTTCTGATATTT
TATGAGGACTGTTGTTCTCATTATGAAGGCATCTGTTATTGAAATGTTCTTGTGCTGG
 TGACTGCGAGTACATTCAAACAAAGAAACGGCAAGAGATTAAAGGCGCCAAAGTTCACTGTG
 CCTCAGATCAACTCGGATGTCAAAGCCGGAAAGATCATCGATCCGTAGGTTCAATTGTGAAATG
 TCCAGCAGGATGCTCAAGACGCCAAATACCATGTATTATGGCACTGACGTGTATGCATCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGAGGGGAAAAATCTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT
 ATCCCTTACCACGATGGAGAGAAATCCTTTATCGTCTTAGAAAAGTAAACCCAAAAGGGTGTAA
 CCTACCCTACAGCTCTTACATACTCATCATCGAAAAGTCCAGTGCCTCAAGCAGGTGAGACC
 ACAAAGCCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAAGGCCATCCCCCTCTG
 CTGCTTCTACCACAGCATCCCCAGACCACAACTCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTTGGTCCACTGCCACCTACACAAGCAGCAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTACGCCCTGGGAC
 TTGTTCCAAAAGAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTCATTGTCTGTTTTAATTGATGGGAGCACCAGCATTGGCAACAGGCCATTCGG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGCTCCAG
 TGATGGGTGTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACACACAG
 AATTCCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCTGGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGGCCAATGGAACAGAGAGG
 GGGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 TCAAGACTTCCGAGAGAGTCAGGAATCAACATTTCTTTCATCACCATTGAAGTGTCTGTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCAACTTTGCAAAACAGGCCGTGTGCAGAACAAAGC
 GCTTCTACTCGCTCCAGTGCAGAGCTGGTTTGGCTCCCAAGACCCCTGCAGCCTCTGGTG
 AAGCGGCTGTGCACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAATCGCGTGACAT
 TGGCTTCGTATCTGACGGCTCCAGCAGTGTGGGACCGGGCACTTCCGACCGTCTCTCCAGT
 TTGTGACCAACCTACCAAGAAGTTTGAGATTTCCGACACGGACACGCCATCGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTTCGACAAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCAGCAGCACGGGGGCTGCCATCA
 ACTTCCGCCCTGGAGCAGTCTTCAAGAAGTCCAAGCCCAACAAGAGGAAGTTAATGATCCTC
 ATCACCGCAGGGAGGTCCTACGACGACGTCGGATCCAGCCATGGCTGCCATCTGAAGGG
 AGTGATCACCTATGCGATAGGCGTTGCCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCCGCAGAGACCACTCTTCTTTGTGGACGAGTTTGACAACTCCATCAGTATGTC
 CCCAGGATCATCCAGAACAATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTCCAGAG
 CAGGCAGAGCACAGCAAGTGCTGCTTTAGTAACTGACGTGTTGAGCACCCCAACCGCTTAA
 TGGGGCAGCAGCAGGTGCAATCAAGTCTTGGGCAGGGCAGTGGAGAAACAAATGTCTTGTATT
 TTCTTTGGCCATATGCTTTTTCATATTCCAAAACCTTGAGTTACAAAGATGATCACAAACCT
 ATAGAATTGAGCCAAAGGCTACATCATGTTGAGGGTGTGAGAGATTACATTTTGACAATT
 GTTTTCAAAATAAATGTTTCGGAATAACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTTCTGATTGAACCTCTGTAACCCCTCAGCAAGTTTCTATTTT
 GTCATGACAATGTAGGAATTTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAATAAAAA
 AAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA
 AAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA

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MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKAVAGQSGYKGSYNGVQSI
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAQAQGETTKAYQRPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHRSQEMDLWSTATYTSQNNRPRADPGIQ
RQDPGSAAFQKPGVADVSLGLVPKEELSTQSLPVLSDGPNCKIDLSFLIDGSTSIGKRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKYVVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPQVLRKVCYDTRLACSKTCLNSADI
GFVIDGSSSVFNGNFRTVLQFVNTLTKLEFISDTRIGAVQYTYEQRDLFVFDKYSSKPD
LNAIKRQYVSGGTSTGAANIFALEQLEFKSKPNKRKLMLITDGRSYQDLEPGIPMAAAHLKG
VITYAIGVAAWAAQEELEVIATHPARHSSFVDEFNLDHOYVPRIONICTEFNSOPRN

CAGAGTAACTGGTTGTCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGCACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCGCTCGGCCCTCTGTGCGCGTGTCTGCCTCAGCACCATGGT
GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAA
TGATGCATGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAAACATT
CGAGTGGTAGGAGGACCTCTGCTGTCTCACTGCTCTCCAAGAGGCTGGGGTGGGAAGTAGA
GGCTGGATGGCCCTGTTCCGGGCCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCC
TCCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
AACCCAGGAGAGACCCCTGTCACTGTACGCGAGGGATTGGGACCTTCATTGTTGAATTTGC
CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
AAGTGGGTGGCCAGGACGCTCAGGCATCGGGCTGGCTGGACCTCTCTATTGAGTACTTGGT
GAAGGAGGCCATCTGCTTCAGGATAAGAAGCTCAGTGGCCATGTTCTCTAGAGTATAACAAG
CCATCCGGAACTACACCCGCTTCGATGACTGGTACTGTGGTTCGAGTGTACAAGGGGACT
GTGTCCATTGCCAGTCTTCCAGTCCCTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
AGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
CTTCGGCCAGAATTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGAT
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
GAAATTTAGAAAAAACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
CTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
AGACTCCTCA**TAA**CCACTGGATAATTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFQSLEAYWPGQLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDP TLLELGRDAVESIEKISKVECG
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSPFTSKLALLGQVFLDSS

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AAAGTTACATTTTCTCTGGAACCTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTCT
GGCAGAAAGGAGGGTGCTTCGGAGGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTTCTGTGCAATACCAAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTGATGTCACCTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
CATTCGTGAAGGCCATTGGGAGGTGACAGCCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCTGGTATCTGCGCCTGTGTTGCTTTGTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTCTGTCTGGAATAAGGGCCGGCTGTCTCAGTACTCCTGTGTCGCCCTGG
TGGTCTCTCCAGACACCTTGAAATAAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCTGAGGAACCTCTCAGGGCCTGGAT
CTCA**TAGG**TTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAAGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACAGTACACATAAA
TACACCCAGCACATTGCAAGGCTAGAGGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAAATGATCAAGGACTCTACACACTGGGT
GGCTTGAGAGGCCACTTTCACAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
TGSCAATGACAGGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTCT
TGTTGGTAAAGTACAGAATTACAGCAATAAAAAAGGGCCACCTTGCCAAAAGCGGTAAAAAA
AAAAA

FIGURE 117

MQTFTMVLEEIWTSLSFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLIMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDDITATVPYNLRVRATLGSQTS
SILKHFFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECCEVQGEAIPLVLALFAFVGFMILIV
VVPLFVWKMRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACCTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGCTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGAGAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGC GGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCTGCAACCAAGTTTGGCCAAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
 TGGTAGGGGCTTGGGACCCAACCTGTGTGAGTGGAGGAGGTCAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTATAACACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGAA
 AAATCTAGTATTTTGATTATTTGAATCTTACAGCAACAATAGGAACCTCTGGCCAATGAG
 AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCCACCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAAGTTCATCCACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTTTCTTCATTACAAAAGAAATGCAAGTTTATTGTAACAATCCA
 ACAATACTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAAA

THESE

MVAATVAAAWLLLWAAACAQQEQDFDYDKAVNIRGKLVSLSEKRYGVSLSLVNVVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKKEPTWNFWKYLVPADGKVVGAWDPTVSVEEVRPQITALVRKILLKREDL

CGGACGCGTGGCGGGGCGGGACGCAGGGCAAAGCGAGCCATGCGCTGTCTACGTCGGGATGCT
TGGCGCTGGGAGGCTGTGCGCGGGGAGCTCGGGGGTCTGGGGGCCGGGCCGCCCTCTCT
CGGAGTTGGCAGGAAGCAAGCATGCTGACGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATGCG
CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAGGGGTGCACCAAAAAGCATCTTA
ACAGCAAGACTGTGGGCGAGCTGCTGGAGACACAGCAGAGGGTCCAGACAGAGAGGCC
TTGGTCGTCCTCATGAAGAGCTCAGGTTGACCTTTGCCAATCAGGAGGAGGTGGACAA
AGCTGCTTCTGGGCTCTCTGAGCATTGGCCTTGTCAAAGGTGACCGGCTGGGCATGTGGGAA
CTAACTCCTATGCATGGGTGCTCATGCAAGTTGGCCACCGCCAGCGGGCATCTATTGGTG
TCTGTGAACCCAGCCTACAGCCTATGGAATCGAGTATGTCTCAAGAAGTGGGCTGCAA
GGCCCTTGTGTTTCCCAAGCAATTCAAGAACCCGACAAATCTACAACGTCTCTGAAGCAGATCT
TCTCAGAAGTGGAAAGTCCGACGCCAGGGGCTTTGAAGAGTCAGAGGCTCCGACATGTACC
ACAGTCATCTCGTGGATGCCCTTTTGGCGGGGACCTGTCTCTGGAATGAAGTGGTGGCGGC
TGGCAGCAGCAGCGCAGCATCTGGACAGGCTCAATACACACAGCAGTCTGTGCTGCCATG
ACCCCATCAACATTCAGTTCACTTCCGCGGACACAGGCAGCCCAAGGGGGCCACCTCTCC
CACTACAACATTGTCAACAACCTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
ACCAAGCAGAGTGTGGGATGATCTGCTGCCAACCCCTCTACCTTGTGCTGGTTCGTTGGAG
GCACAATGATGTGCTGATGTACGTGTGACCTCATCTGGCTCTCCCATCTTCAATGGC
AAGAAGGCACTGAGGCGCATCAGCAGAGAGAGGACCTCTCTGTATGGTACGCCCCACGAT
GTTCGTGGACATCTGAACACCGAGACTCTCCAGTTATGACATCTCGACCATGTGTGGAG
GTGTATTCTGGTGGTCCCTGCACCTCCAGAGTTGATCCGAGCAATCATCAACAAGATAAAT
ATGAAGGACCTGTGGTGTGCTTATGAACAACAGAGAGAGGTCGCTGTGACATCTCGCGCACT
CCCTGAGGACATCTGGAGCAGAGGAGGACAAAGCGTGGCAGAAATTATGCTCACACGGAGG
CCCGGATCATGAACATGGAGGCAGGGGACGCTGGCAAGCTGAACACGCCGGGGAGCTGTGC
ATCCGAGGATCATCGCTCATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGGAGGAAGCAT
GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCCAATGAATGAGCAGGGCTTCTGCA
AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
CTCGAGGACTCTTTTCAAGACACCCGAGGTGACGAAAGTCAGTGGTGGGATGGAAGA
CGATCGGATGGGGGAAGAGATTGTGCTTGACTTTCGCTGAAGGACGGGAGGAGACCCG
TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
GTGTTTGTCAACAACTACCCCTCACCATTTCAGGAAGAATCCAGAATTCAAACTTCAGA
CGAGTGGAAAGCATCTTAATCTCTGAATAAAGCAGAGGCTGTCTGGCCGGTGGCTT
GACTCTCTCTGTGAGAAATGCAACTGGCTTTATGCACTAGATGTCCCGAGCACCAGTTT
TGAGCCAGGCACATCAATGTCAAGGAATTTGATGACCAAGCAATGAAGACTCTGGATGGGT
CGGGAACTCGCTTGGGCACAAGGTGCCAAAGGACGAGGACGCTGCCAGGCCCTCCCTCTGT
TCCATCCCCACATCCCTCTGCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
GAAAAGAAAAAATAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFSSREVDRMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETQAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFQKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDEVVAAGSTRQHLDDQLQYN
 QQFLSCHDPINIQTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCCKIVGRSKDMIIRGGENIYPAELEDFHHTPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCAGTGGAGGC
CATCAGCAGAGAGAGAGGACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

GAGCAGGACGGAGGCCATGGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
AGGCTGGCTGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
GTGGACGCTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
AGTGCGGGGTTGCGGTTTCGGACTCCCCGGCAAGAATGACCGCGGCTTGGATCTTACGGGC
TTCTGGCGTTTCATCCAGCTGCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGCTGGAGTG
CTACAGCTGTGTGGGCTTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTAGCT
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
GCTAATGTGACTGTGTCCTTGCTTCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
TGGAGTAAACAGGCCCAGGTTTCAGCTGACGTGGCTCTGTTGCCAGGGGTGCCGCTGTAAT
TGACTCTCGCAACAAGACTTACTTCTCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT
CCAGAGCCCACGACTGTGGCTCAACCACATCTGTCAACCATTTCACTCTCGGCCCAAGTGAG
ACCCACATCCACCACCAAAACCATGCCAGCGCCAACACAGTCAGACTCCGAGACAGGGAGTAG
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAG
CGCAGCAATTACGGGCAGTATCCTGCAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTG
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTCTC
CATACTTCTCTGTTCCACCAGCTGGACTGGGCTGGCCAGCCCTGTTTTTCCAAATTCCC
CAGTATCCCCAGCTCTTGCTGCGCTGGTTTTCGGGCTTTGGGAAATAAAATACCGTTGTATAT
ATTCTGCCAGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGPTC
TCCGCTTGTCCTCTTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACAGGGGAAGGTG
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
GGTGGGTGGGACAATGGCTCCCCACTTAAGCACTGCCTCCCTACTCCCCGCATCTTTGGG
GAATCGGTTCCCATATGTTCTCTCTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTAC
CCAATTGCGCCCTATAGTGAGTCGTA

MDPARKAGAQAMIWTAGWLLLLLLRGGAAQALECYSCVQKADDCGSPNKMKTVKCAPGV DVCT
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLT SRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCFCGDNVTLTAA NVTV
SLPVRCGVQDEFCTRDGVTGPFFTLSGSCCQGRSCNSDLRNKTYFSPRIPLVRLPFPPEPTT
VASTGVTSTTSAPVRPTSTTKMPKPTASQTFRQGVHEASRDEEPRLTGGAAGHQDRNSG
QYPAKKSGQPPHNKGCVAPTAGLAALLLVAAGVLL

[illegible]

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRRLLEPLDANVDA

0998923 41204
100211-55268660

AAACTTGACGCCATGAAGATCCCGGTCTTCTGCCGTGGTGCTCTCTCCTCTCGTGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAACGGCAGCCCTCTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTCCATCCAA

FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLFFLNWDAFPKLKGLRSATPDAQ

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CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACGACCCATGGGGGTGGAGATTGC
 CTTTGCCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
 TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
 TTTGCGGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
 TCATGATTTAATAACCATCCTTGCGAAGTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
 AATTTTGTATTACTAGATGGCTTCCATTATCCACCCTATTTTAAGGTCCCTTTATTTTT
 AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
 TTCATCTATTAATTGTAAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
 TATCCCTGGGTGCCCTGACACATTATGTAGTGATCCCCAATAATGTGATTGTTAATTTTCT
 TGTATTCTAATATTAGTACATTAGTGTGTGATGTAATGAATAACCAAGATATTTTCTT
 AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAGACTGAATAGTGATG

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCC**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTATTGACCAAATTAACAGGTCCTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTCTAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGGTGGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGTTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTGTCTCGGAAAAACCAAACTTGTTGATGCAGAATACACCAAAAAAC
 CAGGCCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAATACAAGTATCTGTTTAATTTTCCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGATGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAAC**TAG**TAGTCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTGAACCAACTCTACCTTTTCACTTTCTTAAGCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCACTTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTTATTTTAATGTAGG
 AAACCCATGCGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTCTCTTTTGTAAAACCATAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAGGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFDQINRSLENYEPCCSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYRENDCMFPSSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPFIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLFNFRGVAASFRFKHLFLCGSLVFHVGD EWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSY
NVTRRKG YDQII PKMLKTEL

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CACCCCTCCATTCTCGCC**ATG**GCCCTGCAGTGCCTCTGTACCTGCTGCCCTGCCTCTT
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAG
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTCAG
AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTT
GACTATGCTGAGCTCATGGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
TTCCTCCTTACCTCTACCTGGGCCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGGCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGTTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTTAAATTCTGAGTTTCAGCCA
CTGAACCTCAAGGTCCACTTCTACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCAGTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCTGAGAAGGAAAGGATCTGCC
CTGACCACCTCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCTTCTGACCCGCT
GGCTTCCACTCCAAGAAGGTGGACAGGGTCTGCAAGTCTCAACGGTCATAGCTGTCCCTCA
GGCCCCAACCTTGCTCACCACCTCCCGCCCTAGTCTCTGCACTTCTTAGGCCCTGCCCTC
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACCTCGATGACTTGGGGCTC
CCTGCTCTCCCAGGAAGATGCTCTGCAGGAAAAATAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFTSLRPLLGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPKGPV
LWEARAEFWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVVPTLGTDRLLLAFLLLTYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

CCGAGCAGCAGGAGATTCGCTGCGTTTAGGAGGTGGCTGCGTTTGTTGGGAAAAGCTATCAAGGA
AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTACAGTAGTTCACAACAGATCTGAGTGT
TTTAATTAAGCATGGAATACAGAAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATT
CCACAGTTTTCTTAGCTCCCTGGACCGGTTGACCTGTTGGCTCTTCCGCTGGCTGCTCTA
TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
AGCTGCTGTGGAATGCGCTCGGCTCTCTGGAAGTGTCTTCCGAGTAGGATGTCACTGAGATCC
CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATT
ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATT
CTGGTCATTCTGGTGACCTCCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
TTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTCTAGAGGATGAACACCTTCTTTATGGT
GACATAATCCGACAAGATTTTTAGACACATATAATAACCTGACCTTGAAAAACCATATGGC
ATTCAGGTGGGTAACTGAGTTTTGGCCCCAATGCCAAGTACGTAATGAAGACAGACAGCTGATG
TTTTCATGGAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT
TTCACAGGTTATCTCTAATTGATAATTATTCCTATAGAGGATTTTACAAAAAACCCATAT
TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAGAACCCATCAAGTTT
GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTTCATATCCAGAGA
CACAAATCTTTCTTTCTATATAGAATCCATTGGATGTCTGTCAACTGAGACGTGTGATTG
CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACC
ACATGCCATTATTAACCTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
GTGTTAAATAAAGTAGGTACTGTGGAATAATCATGGGAGGTCAGTGTGCTGGCTTACACTG
AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAGAAGGAATTGGAGGTTTTTGTGAAA
GAAATTAATAGGACCAACAATTTGGACATGTCACTTCTGTAGACTAGAATTTCTTAAAGGG
TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTTATTATTG
AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
TGTAGTCTGTGTCAAAAACCTTCTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
CATCTTTTACATGCAACATTTTCCAGTTACTTAAGTCACTGAGTCAGTTATTATTATGATACATC
TCCATTATAGTAAAGTCATAGTCTATTATGCTATCAGTAATCTCTGGACTTGTTTAAAT
ATTTTACTGTGGTAATATAGAGAAGAAATTAAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQAEK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYPYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNQFAATRLRFQKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGKGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

CAATTCTGAAACTAACTCGTGTGCAGAATTGACCTTTGAAAAGCATTGCTTTTTTACAGAAGTATA
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCTTAGTATTAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATTAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAGAAGCTGGTTGTTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAAGCTCCAGCCCTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCC
ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCAACAATCTCCATTAATGTGAAGACAG
TCAAAAAAGAACCTTGAGGATAGACACAGCCCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAGTCGATCGAGGTCAAGAACACGATCAGC
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCGCCGAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAACAGCAAACCTGATTAGGATTTGATTTCTTGAACCCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCTTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT
ATACAGATAAAAATTGCAGACACTGTTCTATTAAAGTGGTTATTGTTTAAATGATGGTGAAT
ACTTCTTAAACACTGGTTTGTCTGCATGTGTAAGATTTTTTCAAGGAAATAAAATACAAAT
CTTGTTTTTTCTAAAAA AAAAAAAAAAAGT

MNDSLRTNVFVRFPQETIACACIYLAARALQIPLTRPHWFLFGTTEEEIQEICITELRLY
TRKKPNYELLEKEVEKKRVALQEAULKAKGLNDPGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVTKVKEPEDRQQAOKSPYGNVRKDSKRSRNSASRSASRSRSHSRHTPRRHN
NRRSRGTYSSRSRSHSESPPRRHHNGSPHLKAKTRDRLKSSNRHGHRKKRSRSRQ
SKSRGSDHSAKKHRERGRHHRDRRERSFSERSHKSKHHGGRSGHGRHRR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTT TAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAGGGCTTCGCT
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGATT
GAATCCGGATGGAAGCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

GGACACGAGGCCCTCGTGCCAAAGCTTGGCACGAGGGGTGACCCGCTTCTCGCACGCCTCATGCG
GGTCTCTGGAGTACAGCTGGTGGTGACCCGTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGGAGATGCCCGTTCCAGCTTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCTGCGCTTCTTCTTGAGTACCAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGCTGGGACTGGGCGCTTCCCTGCTGGCCAAAGCTGGCTATCCCGGTG
GGACTTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCTACCTTCCCAGGCTGCGGCTGGC
CCAGACCCACCGGGAGCAGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACCAGCTTCTGTCTCCCCGTTCATCTGTGGCTCTGGACAAGGCCATTGCACGGGAC
TTCTTGACACAGCCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCTTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGACGCGCTCATCTCACCTCAAAGTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTTGGGGCTTGGGCCAGCTCCTCTACTATCCCCGAGCCCATCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCTTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGGCTCTACTTCCACCAGCACTTGGCA
GGCTCCCTTAGCTGCCTGCAGACCCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGAATCCCC
GGCGTTCCCTTCAACCAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCGCTCA
GAATCTGTTCTTCTGGGCCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTAA

MAVLGVQLVVTLLTATPLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCLPTTVDALVLRFFLEYQWVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVRIRYFSAEEGGERSVCILTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLWLLVVLCLLRLARTRPHLQGLCLAKARVEQLRRREAGRIAREIQQRVVRVYCYVT
VSLQYLTPLILTLNCTLLTLLTKGYSLWGLCAPLLSPDPSSASAAPIGSGEDEVQQTAAIRI
AGALGGLLTPLFLRGVLAYLWTTAACOLLASFLGYLPHOHLAS

FIGURE 145

CGTTNGCAGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

AATGTTCTCATCTCTCATCAAGAGATCAGAGACATATCTTCTTACGGGGCCGFGATTTATTAAGTGCGCTT
AATCAAGAGGTTCTCACTCAAAATTTCTTGTCGATCTACTGATTTCTTGCGGGCATGCCAAGGTTTGCTTTAAAGAGG
TTGGCTGTGTTTGGGCCCCTTGACTCAGACAGAAGTGCCACGGAGAATGCAGACACTGCTCGGAGATGAGG
CGCTCTGTGTTGCTGGTCTTGCTTGGCTCGTCACTGCTAACTACATTCAGACATTTGGGCAAGCTGCACTCTCTG
TATTCAGAACTCTTAAAGGTGCTTCCACTACGGCTGCACAAAGATGAAGAGAGCGCTCAGACAGATGGCTG
TCGACAGCGGCTGTGGCGGCTCAGACGAGCGGCTCCTCCCGAGAGTTTTCGACGTGCCACCATCTCCTTAT
TCAGACAGGAGCGTGGCTAGACAAACCTCGTCTACGTGTCTTCGCGAGAGAGGGGACGAGCAAGTACGCCCA
GTGGACTCTGCGCCGAGCTAGCAACGCAACTAGGGCAGCGGCCCTTTGAGAGATCCCATATTAAGACAGATCAITTTAA
AAAAATTAATCGGAGTTTGAGTTGTTCTTCGAGGACAGAAAGCGGGAGTCAGTTGCCAAGTCTCGCGAOCAG
CGAGGAAAAATTTTGAARACACCACTCGCCCTGAAGTCTTTCCAAGTTGTACCCACTGATTCAGATGTGGTAA
ATTACACAGCTCAAGATCAATCGATAGTATCCAGTGAAGCGTCTCATTTAGGCTGTTGGAGGTATGCGAAAC
CCCACTGGTCCATATCATTTACCAACATATTTGCTGATGGGTGATCCGCCAGAGACGGCCCGCTCATGCCAG
GAGACATCATCTAAAGGCTCAA GGGATGGACATCAGCAATGTCCTCAGCAATACGCTTGCGTCTCTCTCGGG
CAGCCCTCGCAGGTGCTGTGGCTGACTGTGATCGTGGAACAGATCTCCGACAGGAAACATGGACAGGCCGCC
GGATGCTCTACAGGCCCGAGATGACAGCTTTCTATGTGTTTCAACAAAGATGCCGCCGAGGACAGCTTTGAA
TAAACTGGTGCGCAAGGTGGATGAGCTCGGGGTTTTCATCTCAATGTGCTGGATGCGGTGTGGCATATCGA
CATGGTCAGTTTGAAGGAATACGGCTGTGTAGCCATCAATGACATGATCTTCGATATGGCAGGCCAGAAAG
CGCGCTCATGTGATTGAGGCAGCTGAAGACGTTTTCACCTCTGCTGCTCGCCGCGAGCTTCGCCAGCGAGCC
CTGACATCTTTCGAAGAGCCGCGTGAACAGCAATGGCAGGTGTTGCCGCGGACAGGGGAGAGCAACATCT
CCAGGCCGCCCTCCATCTCAACTATTCTTGTCATGAAGAGGTTGTAATATCCAAAGAACGCCCGGTTGAATCTCT
CGCATGAGCCTCGCAGGGGAGCATACATAGAGAATGGATTTGCTCATATGTACATCGATGTTGAGCCGCG
GAGGATGATCAAGCAGAGATGGAAGAAATAAAACAGCGATCATTTGTGAAITGGATGGGTGGCTGCAACTGACA
GAGGTCAAGCGGATGAGGCAGTGGCAATTTATGAAAGAACATCACTCTCGTAGTATCAAGCTTTTGAAGT
CAAGAGATGATAGCCCCAGGAAGATCGACAGCAGCCAGCCAGCCCGTGGACTCCAAACACCAACTGGCCCCACCA
GTGACTGTCGCCATCTGGGTGATGTGGCTGGAATACACCGTGGCTGTATTAATCTTAAAGATATTTGTAAT
CAGAAAGAACACAGCTGGAAGTCTGGGCTCTGCATTTGAGGAGTATGAAGAATAACATGGAACAAACACTTT
TTTTCATCAAACTCAATTTGGAAGGAACACCAAGCAACAATAGTGAAGAAATAGATGGTGGTGAATCTTCTT
CTGCAATGGTGAAGATACATCAGGAATGATACATGCTGTTGCTGCGACAGTCTCGAARAGATTAAGAGAGA
ATTACTCAAACTATGTTTCTTGGCCTGGCACTTTTTATAGAAATCAATGAGTGGTTCAGGAGAAACAGAAAA
TCCAAATGAGCAAGAGTGAARACATATATTTCTGTGAGTTTATATTTAAAGAGAAATACATGT
AAAAATTCAGGAAAGATGATCATCTATCAATGAAGCCAGTTACACTCAGAAATATGATTCAAAAAAATTA
AAACTCATGTTTTTTTTCAGTGGGAGATTTCTCATTAATCTCAACAACTTTTATATTTTTTTCATTCAT
AAAAAGCCCTAAAAACCAATAATGATTTGATTTATACCCCACTGAATTCAGCTGATTTAAATTTAAAAAT
GGTATATGCTGAAGTCTGCACAGGGTACATATGGCCATTTTATATTCAGCTCAAAATATTTTTTAAAAATGCA
TTGCTGAGAAACGTTGCTCTTCAATCAACAGAAATAAATATTTTTCAGAGATTTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDKRKRSDGCPDGCASLTAT
APSPPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENNTAPEVFPRLYHLIPDGEITSIKINRVD
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRS
PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISR DGRIKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPFIFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

147/330 147/330

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTGTGTTTATCTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAATTCTTTCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 150

GGACAGAGCCAGGAATAGGAGGTTCTACTGCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG
 GCCGCTGGGTGCTCATAACTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCTTCCT
 CAACCTCAACGTCACTCAAGTCCAGTCAGACTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCCGGCCAACCTCACTCTGCAGGACAGAGGGGCAGGCCCAAGGTTGGA
 GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTCGCCG
 AGCCAGACATCGGACTGGTTCGGTGCCAGGCTGCAAAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTGGAGA
 GCCCCATCCTTGCCCTGCCCTCTACAGGAGCACCCCGCTCTAGTGAAGAGAGTATTGGG
 GGGTTCAGGATAGGGAATGGGGAGTTCAGGAGCACCGCAAGCAGCAGCCATCT**AGAA**GAAC
 GTCCAGAGAGCCAAGCAGCGCAGGAGGTGACGGCCATCAGCGTGCATGTTCTGATTTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPIITNSLIGKDQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

GGTCCCTTAATGCGCAGCAGCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGT
CTGTCCGGCTGGTCCC GGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCAGGTTGGTGTGCGGTTCAAGGCCAGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCAACCTGTCAGTCCCCTGGGAAGAAA
CTAAATGTCAACCGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC
AGGCAAGGATGCTTGTGTAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCACT
TTCGATGGCGACATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCACAAGATGAAAAGAAAGTGGGAGACTGACAAGGTTGTGGCCATGTCCTTCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCAC
CTGGAGCCAAGTGCAGGAGCACCACTTCGCCATGTCCTCAGGCACAACCAACTCAGGGCCAC
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
GTCCTTGATCAAACCTGCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCTT
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTTATGCAATTTTCTCTTGGTGCTAC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTT
TCTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAATGATATT
GTCAGTAAAAATACAGTTAGACTTCAGACCTCTGGGGAATCTTTCCGTGTCTGAAAGAG
AATTTTCTTAATTTATTAATAAGAAAAAATTTATATTAATGATTGTTCTCTTCTAGTAATTTAT
TGTTCTGTACTGATATTTAATAAAGAGTTCTATTTCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCACVQGVDEKFTL
HYDCGNKTVTPVSPLGKKNVTTAWKAQNPNVLEVVDIETELQRLDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMS FHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTOLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAGTTATATACCGTGGAA**ATGG**GAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAAACAGGACAGATTATTTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTG**TAA**TCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCCTGTAT
CATCCTTTTCAATAAACTGTATTCATTTTGAIAAAAAAAAAAAAAAAAAAAAAA

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTTGGCAGGTAACCTGTGCACCACCACACCTGGAAATGCCATCTCTGCTCCCGTTCTGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGGCTCGTGCAGTAACCAAGTTCAGCAAGTGGTGTGCACGCGCCCGG
 GGCTCTCTCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCCTCAAC
 ACCCTGGAGCTGTTGCACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTG
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCCTTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCTTGAGATCAGGCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG
 AACTCAGAGGTGAGCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACT
 CAACTTGGCCCAATAAACCCTCTCTTCTTTGCCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCACTGCTCCCAT
 GCACATGCGAGGCCCTACCTCGTGGAGGTGGACCAGGCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGAGCGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACTTTTCACAGTCTGTGC
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGAGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCAGCGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCCGAAAGTACAAGCCTGTTCCCTA
 CCAGCTCCACTGGTTACCAGCGGCATATACCACCTCTACCACGGTGCTCATTCAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCCACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAGACATCCAGCAGCAACATCCCG
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGCGAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACTACAAACACCTACAAACAGCACATGGGGGCCACTGGACAGAAAAACAGC
 CTGGGGAACCTCTGCACCCACAGTCACCACTATCTGAACTTTATATAATTACAGACCCA
 TACCAAGGACAAGGTACAGGAACTCAAATA**TGACT**CCCCCTCCCCCAAAAACCTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAAAAATTTAAAGA
 CAAAAAGTCAAAACA

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 100211-2000000

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAATAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFPPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSSVKWL LPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LN TSNYSFFT TTVT VETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLRKRHHQORS
TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSGEGAVVLP TIHDHINYN TYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

10024-66666

[illegible]

MELGCWTLQLGLTFLFQLLLISSLPREYTVINEACPGAAWNIMCRECEYDQIECVCPGKREV
 GYTIIPCCRNEENECDSLIIHPGCTIFENCKSCRNGSWGGLTDDFYVKGFYCAECRAGWYGGD
 CMRCGQVLRAKPGQILLESYPLNAHCWTIIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
 GDNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
 TCVLDKAGSYKCACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
 VSFFCNNSYVLSGNEKRCTCQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVSRETPLH
 QLYSAAFSKQKLQSAPTCKPALPFGDLPMPGYQLHHTQLQYECISPFYRRLGSSRRRTCLRTGK
 WSGRAPSCIPICGKIENITAPKTQGLRWPPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
 RTVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
 ADIAILLKLDKARISTRVQPICLASRLDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRS
 VSVVDSLDDCEEHDHGIPVSVTDNMFCSWEPETAPSDICTAETGGIAAVSFPGRASPEPR
 WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKFDIERNMK

ACACGGCATTGTGATCTCAGTTGTGCATCAAGTTCCGCAATCAGATTGGAAAAGCTCAACTCACTT
AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGC
TTCAACCTGACTTTCCACCTTTCTTACAATATCCGATTACTGTTGCTGTTGACTTTGTGCCT
GACAGTGGTTGGTGGGCCACCAGTAACACTCTCGTGGTGCCATTCAAGAGATTCTAAAG
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGAAAACTCTGACT
AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
CCAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTTACAGAGGGTCGCCATC
CTCGTTCCCCACCGGAACAGAGAGAAACCTTGATGTACCTGCTGGAACATCTGCATCCCTT
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
TGCTTTATATTCACAGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTA
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCAGCTGGGTACAGGTTACGTTACAGTG
GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGACGACTTTTTCAAGGTGAATGGATTCTCT
AACAACTACTGGGGATGGGGAGGCAAGACGATGACCTCAGACTCAGGGTTGAGCTGCCAAG
AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCACGAGTCTGG
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATAGTATCTGTGGAACACAATCCTTTATA
TATCAACATCACAGTGGATTCTGGTTTGGTGCAATGACCCCTGGATCTTTTGGTGATGTTTGG
AAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT
CCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
AAAATGAACGCTATTGAGGACTCTGGTTGAAGGAGATTATTTTAAATTTGAAGTAAATATAT
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT
GTGAAGTGGTGGTGTGAGGTGAGAAGCGCTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCCTCAGGGGAGGACCTGCCCAGGTATGCCT
TCCAGTATGCCACCCAGAGATAACACTCTCTATTAGTTTTTTTAAAGAGTTTTTGTAAATGA
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTTACATATTAACTAATAATAATA
TGCTCTATCAAACTCCTGTGAGTAAATGTGAAAAAGCAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTLCITVVGWATS NYFVGA IQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTGCGCAGCGGGCTGTGGGCGCGCCGGAGGAGCACC GCCGCAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGTCCGGGCCCGCA**ATG**
 GCCCAGGCAGTGTGGTCCGCGCTCGGCCGCATCCTCTGGCTTGCCTTCCCTGCCCTGGGC
 CCGGCAGGGGTGGCCGAGGCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCCCACCTTACCCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCCGCCACCTGCCCGGGGAATCCCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTTCCCATCACAGAGTTCCTCGTGGGGGACCTTGTGTACCCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCCCTGAAAGTCTCCTTCCCTCCACGACCCGA
 GCAACTTCCCTCAAGACCGCCTTGTCTTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCCTGAAGCT
 CAAAGTGGTGGCGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAAACCCCTTCGAGGCATCCAAGTGTGGGG
 CCCACCCTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGATGCCACC
 CTGTGTCGTGGCCAGCAGCGTACAACCTGACCCACCCCTTCAGGACCCTGGGGACCTTAC
 TGCTTACGATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTGTCTTCCCATGTGCTACACTTATCAGTGTGA
 TGTGGCCTTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAAGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTGTGT
 GGAGACTCCATCTGAGTACCTGGAAATTTGCTGTGAGAACCACGGGCTGTCCCGCCCTCT
 ATAAGTCTGTCAAAACTTACACCGTG**TGA**GCACCTCCCTCCCAACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGAGGGGTTCATT
 TGGCTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTACGCCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGACGAGCT
 TTGATGCTTGGGGTGTCCGTGTGACTCCTAGGTGGGCTGGCTGCCACTGCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTCTCTAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGATGTACACACACACACACACACACACA
 CACACACACACAGAAATATAAACACATCGCTCAGATGGGCATTTCAGATGATCAGCTCTGTA
 CTGGTTAAGTGTGGTGTGCTGGGATGCACCCCTGCATAGAGCTGAAAGGAAATTTGACCTCA
 AGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCCCTGGATGGGGGGCAGGACT
 AATACGTAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTATCGAAACCCATCTGTG
 AAACCTTCACTGAGGAAAGGCTTGCAGCGGTAGAAGAGGTTAGTCAAGGCCGGGCGCGG
 TGGCTCACCGCTGTAATCCAGCACCTTGGGAGGCCAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCACCTGGCTAACACCGGTGAACCCCGTCTCTACTAAAAAAATACAAAAGTT
 AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCAACCCGGAGGCGGAGCTTGCAAGTGAAGCCAGATGGCGCCACTGCATCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLWPSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIIGFTVKLVVAEWEVEPEPATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

[illegible]

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

100211-66268650

CTGTCAAGGAAGGACCATCTGAAGGCTGCAATTGTTCTTAGGGAGGCAGGCTCGGCTGGCCTGGAATCTTCCACCAATGCTCTGTGGCTGCTTTGATAGCTGATGTCGACCCATCTTGGGCAATCTCCCTGCTCTTCCACCTCCTTCTCGTTTTCATAGTGTCGACCAATTTTGGAGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTGTAATAATCTTTGCGTGGGCTACCTTGAGATCTGGAGCGAGGACCAAGGAGAAGCAACCACGCTTTACAAGCCCTACACCAAGGAATCATTTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGATCTGCTCGAAGTGGTAGTAGTAAGGCTCTGCAGCAACCTCCAGAGTTCGAGCTCTGACATTTTCTACTTTTTCGGAGAAGGAATGGAGACCAATTAGGATGATGAGGTGACAAAGAGATCTCAGCAGAAGAAGCTGAGTCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCACGGCTCTGGGGGCTAGGAGTGCTGATTCGGTATCTGTTCTGCTGCCCTCAGGATAGCACTGGCTTACACGGGATGACCTTCTGGTGGTGGGCAACCTGTTGGGATACCTGCCAAATGGGAGGTTTAAAGAACTCATAGTAACAATGTTCACTTAATGTGTTACCGGATCTGCTGCGAGCGCTGACGCCATCATCACTACCATGACAGGAAACACCAAGAATGTTGGCATCTGTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTGGCCACGGATGGCTATTATGCCATTGTTGGGTCAAGTGCAGCGGGGACATGGGTGTGATTTCAGAGACCGATGGTGAAGCGCTGCCACAGCTGCTTTGAGCGCTCGGAAGTGAAGGATGCCCACTGGTGGCTAAGAGACATGACTGAACATCTGCAAGATTAAGAGCAAGCTGCTTCTCTCATCTTCCCAAGAGGAACCTGCATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCTGTTGCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGTTGGTACGCTAGCTGCTGCGAATGATCAACGAGTGGGCACTGTTCTGACGGTGTGGTACTGCTCCCATGACTAGTAGGACGAGATGAAGATGCTGTCAGTTTGGCAATAGGTTGAATCTGCTGATTGCCAGGCAGGGAGGATTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGCTGAAGGACACGTTCAAGGAGGAGCAGAGAGATGATCTGTGGGAACCAACAAGGACAGAGCGCTCTCGAGCCTGCCCTCAGCTGGCTGGGGCACCCTGCGGGGTGCCAAACGGGCTCAGAGCTGGAATGCCCCGCGCCCACTGCTGTGCTTTCCAGACTCCAGGCTCCCGGGGCTGCTCTGATCCGAGACTCCGGCTTCCGCGAGCCGACGGGATCCCTGTGCACCCGCGCAGCCTACCTTGGTGGTCAAAACGGATGCTGCTGGGTGTTGCGACCCAGGACCGATGCTGTTTCTTTCATAAAGCTGCTGGAGAATGCCATTAAGTGAATCTCCCACTTTGACAGCTGCGGGCTGAGTGGGAGATGTGCCATGTCTTGTGCTAGAGATGGCGCTACAAGAGTCTGTTATGCAAGCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCCTCTCCAGGAAAGGCACAGCTGAGGCATGTGCTGGCTCGGCTCAACATGCCCCGACCTTGAGGAGCTCTGCAGACATGATAGGAAGGAACTGTCACTGCGAGGGCTTTCAGCAAAATGAAGGTTAGATTTTATGCTGCTGCTGGGTTTACTAAAGGGGGGAAGAGGCGAGGTGGCGCTGACTGGGCCATGGGGAACAGTGTGTTCTGACTCAGGCTAACCTGAACTCCCATGTGATGCGCGCTTGTGTAATGTGTCTCGTTTCCCCTATCTGTAATATGATCGGGGGGAATGGTGGTATTCATCTCACAGGGCTGTTGTGGGAGTTAAAGTGTGCGGGTGAAGTGAAGACATACAGTTCAGTTTCTTAAGTAGCAGCCCAAAACGGGCGACGGCAGCGCTGAGCTCAGAGCTGCTGCATCGGGCTTTGGATTGTTCTTGTGAGTAATAAACTGGCTGGTGAA

FIGURE 167

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIIVPAIFGV SFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLR LTVLWGLGV LIRYCFLLPLRIALAF TG
ISLLVVGTTVVG YLPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRP RGGICVANH
TSPIDV IILASDGY YAMVGQVHGGLMGVIQ RAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMT SWAIVCSVWYLP PMTREADEDAVQFANRVKSAIARQGG LVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS



GCCCTCGAAACCAGGACTCCAGACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCAG
 ACCTGGCAGGCCAGGCTGTTCCACCATCTGCCCTGGGCTGGCTCCAGACACCTTTGA
 CGATACCTATGTGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCACCATGCCCTGCTCGGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTCTTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGAGCTGGGGAGGTGGTGTCCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCTG
 GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTGAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCTTGTGAGAAGCAAGAATATGGTTCGGACCACGCCCTAGCAGCCTCTCCCCAACAGG
 ATGTTGGCTGGGAGGCCACAGCAGGCTGAGGGAACCTGCACTGTGATGGGGACTTCTCT
 GGGACAAGCAAGGAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVFRRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCTGTCTCCTGTTGGTGCCCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAAACTCCTAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACATAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCTGTGGAATACCGAAAAAGATGGAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVS RNFS SPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENT EYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLTMPDTPRLFAYENVI

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CTGTGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAGAGAGCTGGTCCGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACCATA
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAATGAAGAAGATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGTCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATATGGGTCCATCCTCCCATATCCTGGAGATGGGGAG
AAAGTGATATGACCTTTCATCTGCGTTGCCAGGAACCTGTGCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCCTCT
GTGTCCTCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGCGGGAA
ACTCCTAACATATGCCCCCAATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAACTCTTAAAGGAAGATCTCAGCAAAATACGGGTTTACTCCATGTGGAATACCGAAAA
AGATGGAAAAATCCCCACTCAGTCTCAGATCGGCAGACACCAAGGCTATTGTGCTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTGGAGCAAATCCATGCTCTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACCCCTTGACAAAT
TTTTCATGAAATATTCTCTCTCTGTTCATAAATGATTACCCCTTGCACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLS DIKERFAQLCEEHGILRENIIDLSNANRCLQARE

03569223.112004

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCACTGGTGGTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAA

FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDFSEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

GTCTGAATCCAAATCACTCATTGTGAAAGCTGAGCTCAGACCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCACAGCTGTGCTTCTGAGATCAAGCTCTTCTATTCTTAAGTGAAGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATGTTTAAAGAACCGACTCTCATTTGAAAAGTCTCGTGGAAATAGTGAA
AAAAATGGGTGTCTGATGCTGATAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACAC
CTGATCTTCACTAAAAATGTAAAGTTTCAACAGCTGGCTTTAAATTAATCACTGCTGCCCTG

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

GGGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCCT
 TGGCTGGGCCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC
 AGTGTTTCCACAGCCCCCAAACGGAACATGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGATCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTTCATCGTTTTATGCCACCTTGACACCATCCCGTCTATCA
 CCAATGCCTCAGTGCCTATTGCACCCAAGGATAATCTCTTCATCAGGTTCTTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGAGCGCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTTCACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGCTGGACATGTTTGAG
 CATCATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGAGAGGCGCCATGTAATATATTTGCCACCATTCTGGAGCTCAGTGAGCCCTTGTAGCAAAAA
 GAAGCCAGCATATCTCTCCAGCATATGGACTTTCTGTATTAACCTTCCCATCAGCGGCGGCGC
 TTCCACAGGGCCTGCCGCTGGTGATGACTTTCACAGACGCTGTATCCGGGAGCGGCGTCCG
 CACCTCCTCCACTCAGGATTTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGAGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCTCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
 TTCCTGACCATGTGCTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCGCTTTGACCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCCTTTCTC
 CGCAGGGGCCAGGATGCATTCGGGCAGGCGGCTTCGCCATGGCGGAGATGAAAGTGGTCTTG
 CGTTGATGCTGCTGCACTTCGGTTCTTCCGACAGCACATGAGCCCCCGCAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTTCGAGATGTGCATGAATAAACCGGTGCTGTCAAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFQPPKRNWFWG
HLGLITPTEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFDPAVIRERRRTLPTQGIDDFKDKAKSKTLDVIDVLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESRLHPPAFFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDFFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGLWLRVEPLNVGLQ

000000 112001 10211 2026860

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTCT**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLD SREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFWKYCV

G

FIGURE 185

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCACTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCCAATAAATGTTCAAACCTGTA

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGTGTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGCTGGGTGGTTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAATGTTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTCACCCCTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGCTCTCAGTGGGCACAGCGGTAGGCGGTCT
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGTTCAGGCTCTGGGCTACCTCCATCTCCAGA
 GCATCCCTGCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCACCAAGA
 GCCTCCTTGTTTCATAACCAAGGTTACCCCTACAACCCTGTCCCAACACACCCCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCCACTCTCCGATTGTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCCTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTATCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCTGCCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTCAAGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATATATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTCAACACCTTCA
 ACAGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCA**TAG**TAAGAGCTTCAAGGAAAAC
 CCGAACTGCCATACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGCTGTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCAACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWVFGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPGCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCCAG**ATG**TGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTATTTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCTCTCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTGAG
 GACATTGCCCCCTGTGTGCCACCAAAACAGGACTTCCCCTTGCCCTGGCATCCCTGGCTCT
 CTCCTGGTACCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCCTACCTGAGGAAAAACCAA
 GGAAGCAACAGGAACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
 TGTGGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGG
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
 AACCAGGAAACTAACAATGTAGTTACTAGTGAATACCCCAATGGTTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGGSGME
HRNHLCFCDLYDRATSPPLKCSLL

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CTAGCCGCTCTTGGGCTCTGGGCTGGCGCTCTGGCCGCGCGGCTGGGTGCTGGAGCGAGGACGACGTCA
CCGCACTGGCAGGACATCAAGCTGTTGATTAAGTTGCTCTTGGAGGAGCAATCGGACTGATGCTTTTGATGCTCT
CGATGTGCCCTTCCAAATATACAACAAATACTGACCGGCTCTTGTGTCTTCTTACATCCTTCACCTATCTTC
ATACTCAATAGCAGAGAAATAGTGATGATGACCTGATGCTATGATGAGTAAAGCACTTGCACATCTTCT
TTACAACGGGCATTTGTCGTGCAGCTTTTGGACTCCCTATGTTATTTGTCAGACGACATCTGATTGAGTGGGA
GCTTGTGCTACTTGTCTGCAGAGAAACAGCGATCTTTGCAACTATACTAGGCTTTTCTGTGCTTTGGAAG
CAATGACACTTCTAGCTGGGACGAGTGGCTGAAGAAATAATGACTAATTTCTCAATGGACTTCTGCTGATCT
GTGGGCCATTACGCGACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCGCTCTTGGGGGATTTTA
GGTGTCTCCCTTCACTTTAATGTAAAGCACTACTTATCAACAGAGACTGCTGAAGGATTAAGAGGATTTCT
CTTTTGGAAAGAGCTTGACTGATTACACATTACTATAGTATGTTCTTTGGTGCTGCTGTGAATTAATAAT
TTATGTGTTTCTGTTAGGTTATTTTTTGGAAATCAATGATGCAATGTAAACACTTTTTTAATGATCAAT
TTTGCAATGGTTAGGAATCGAAATTCGCGCGGCTCTTAATCTGCTGCAAGTACATCTTTTCTTAAATTAAT
TAGCTCTCAATTTATACAAAAAATTAATAAAATAGTTTTCAGTCAAGCAGGATGACATCACTCCCAATGTATG
CAGACATACAGACGGGTTGGCATATGCTGTATAGACTGTATACCTAGTCGAAATATAGCTGCATTTATACCTCAGAG
GGCGAAGTGTAAATGCCATGCCCTCGTATAGGGTGTTGGTTTCTGTTGAGACAGATTTTCTGGATTG
AAAAATTTTATGGAATGCTACAGAGGAGTGCTTTCTCTCAATTTTGAAGAATTTATGTAAACCTTA
AGTGAAGGTTGTAAAACATTTTGTAGATAAGTTTTATTTATTTATTTATTTAGTAGGAGTTGCAATGT
GGGAAGAAATGACATGAATTCGATTTTGAATCTGTTCTTAATTTAATAGTGAATTTGTGATCTCCAT
ACCTTTTCATGTTTACCCTGTATAAAATGGACATCAATGGAACCACTGACTGAGGGACAGTGTATGTGCT
ATCATATATGCGAGAAACAACTCTCTGCTCTCTCTTGTACTTTATTTGGTATGTGTATATATACATAAAA
TAATTTTCAAATATAGTTTAAATACATAGAAGTGTTTACTACCTGGAAAAATAAATGCTATGCGGTACAT
CAGAGTGCCCTCCCTCGCAAGGCTCTGCATCAATCAACAGTAACTGTATGCTACAGATAAATATACGA
TTAAACAGTTTAAAGTTTAGACCATGTAATAGTAGTTTCTTATCTCAAGGTTATATCATATGTAATTAAGA
TTTTTAAAGCAAGTTTCTGTATACCTCTGAAGTCTTTGATTTTGAGTTCATCATATAGATGTATGCTGTT
CTTTTAAAGGCGATTTGTGTGTAGTAAATCAAAGTAGGCAAGTCCAGCTATATAGCAGCTTCAGAAAGAA
ACCTGACCAAAAAATCCAGTAACACAGGCATGACAAATTTATAGTGGTCTTTTACATCTAATAAATATCAGGA
CTTTTTTCAGGATGGGTATAAAAAAATCAAGTGGTCTGACAGATTTTGTGAAGATATTTGTGTGATG
TTTATTCAGTATACATACATAAAAAATTTTCCGCAATCAGCAAAACTCAGTAAATCAGACAGCTGTCTGTG
TTTTATGAAGTTTATTTCTCAAGAAATAATGGGAATAATTTGGGATTTGTTCAGCTTTCTAAGATGCTCA
AGGCCAGTATTTTGTGCTCACTTAAAGCATGACITTTAGATATGAGATGACGGGAAGCAGGACAGAAATCG
CGGTGCTGCTGGAGGCTTCCCACTGGAGGCTGAAGTGGCTTGTGTTATTAATAGTTTCAGATTTCAAGAGGA
GGTGCAGGTACACATGAGTTAGAGAGCTGTTGACAGAGTTGGGAAGTCTTTGTGCTGTGATCTGAGCTTT
TTTTTTCAGGAAGATGATCTCTGCTGCTCTCCATTTCTGCTGCGATGTCGAGTGCAGCAGTGCACTGACTG
TTTTATCCATTTGGCCACAGACTTTTCTAACAGCTGGGTATTTTCTATATACTAATTCGATTCGACGACT
GTGCTTTTGACCTTGTATACTAGCTTGACATAGTCTGTCTGATTTCTAGGCTAGTTCATGAGATTAAT
TTTCCATAGAATATGACTGATACACATACCATCTCTCTATGGAAGAAAACCTTTGATGATGAACAAATA
AGTTTTAAATATCTAATTTTAAAAAAA

[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCFQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANA IQFVPVRI FQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRIILNSWKSLSIT
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGA EPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCCTAGTGCCTCCTTCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGCGCTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGGCGCG**TGA**CGGTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

MGVLGRVLLWLQLCALTAQVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHA VSDMLPLD GELVLASGAGFGVSDVGSGLDCGAGEPAVFRSDRFSWHDDPHLWRS GDEA
PGLFFVDAERVPCRHHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAAALLQP

FIGURE 199

[illegible]

[illegible][illegible][illegible]

FIGURE 202

MTSKFILVSVFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQRAHTSGAAMWPGTDVVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

GGATTTTGTGATCCGCGATTGCTCCCACGGGCGGGACCTTTGTAACTCGGGGAGGCCGAC
 GACAGGCCACCCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAGGCAGTCACCCGCAGGGCC
 AAGGTGGCTCCCCTGAGAGGATGAGCAAGTTCTTAAGGCATTCACGGTCGTGGGAGACGA
 CTACCATGCTGGAACATCAACTACAAGAAATGGGAGAAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
 CAGCTCCCACAGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTTGACCTGAAGATCATGTCAGCCGACAGAATAACTATGCTGCCATC
 GTATTCACACTAGCATGAGCATACCAATCTTGGTCTTTTTATGATGGAGAGATCATCTTTAAATT
 ATTTGTCTTCCGCTGAGTTCTTTACCACAAGTTTGAGATCCTGGATGCCCGTGGTGGTG
 TGGTCTCATTATCCTGGACATTGTCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCACTGCTCTGAGAAGCCCTGGACTTGATGAGTTTGTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAGTCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCAATCTCAGATTACAATTACACAGAGCATCTGCCTGTTTCAATCACAAGAGAACAAAACC
 AAAATCTATAAGATATTTCTGAAATATGACGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMASKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARTINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT
GCTCTGTCTGTGCCTGTACGTGCCGGTTCATCGGGGAAGCCCAGACCGAGTTCCAGTACTTTG
 AGTCGAAGGGGGTCCCTCGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCTCCACCTACCGCCAGTGGGAAGCAGAAAAATTGTACAAGCTGGAGATTAAGGACCT
 TGATGGGCAGCTAGACTTTTGAAGAATTTGTCCATTATCTCCAAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTTTAAGATTTTGGACAAAAAAGAAATGATGGACGCATTGACGCCGAGGAGATCATG
 CAGTCCCTGCGGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAG
 CATGGATAAAAAACGCGACGATGACCATCGACTGGAAACGAGTGGAGAGACTACCCACTCTCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAGCATTTCCACGATCTTTGATGTG
 GCTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTG
 GAGACACTGTGTGGCAGGAGGTGGGGCAGGGGCCGTATCCGAAACCTGCACGGGCCCCCTGG
 AGAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGT
 GGCTTCACTCAGATGATTGCGAAGGAGGGGCCAGGTCACTCTGGCGGGCAATGGCATCAA
 CGTCTCAAAATTGCCCCGAATCAGCCATCAAAATTCATGGCCATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACAGGAGACTCTGAGGATTACAGGAGGGCTGTGGCAGGGTCTTGGCA
 GGGCCATCGCCAGAGCAGCATCTACCAANTGGAGGTCTGAAGACCCGGATGGCGTCCG
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTTACAAAAGGCTATGTCCCAACATGCTGGGCATCATCCCCATGTCCCGCATC
 GACTTGCAGTCAAGAGACGCTCAAGAATGCCTGGCTGCAGCAGTATGCAGTGAACAGCGC
 GAGCCCGGCTGTTTGTGCTCTGGCTCTGGCCACTGTGGCCACTGTGGCCAGCTGG
 CCAGTCAACCCCTGGCCCTAGTCAGGACCCGGATGCAAGGCCAAGCTCTATTGAGGGCGCT
 GCGAGGTGACCATGAGCCAGCTCTTCAAAACATATCCTGCGGACCCAGGGGGCCCTCGGGCT
 GTACAGGGGCTGCGCCCACTTCTATGAAGGTTCATCCAGCTGTGAGCATCAGCTACGTGG
 TCTACGAGAACCCTGAAGATCACCTCGGCGTGCAGTCCGGG**TGA**CGGGGGGAGGGCCGCCCG
 CGAGTGGACTCGCTGATCTGGGCCGAGCGCTGGGGTGTGCAGCCATCTCATTTCTGTGAATG
 TGCCAACTAAGCTGTCTCGAGCCAAAGCTGTGA AAAACCTAGACGCAACCCGAGAGGAGGT
 GGGGAGAGCTGGCAGGCCAGGGCTTGTCTGTGACCCAGCAGACCCCTCTGTTGGTTCC
 GGCAGAGACATTTCTGAGTGCCTGCCAATAGTGAGCTTGGAGCTGGAGGGCCGCTTAGT
 TCTTCCATTTCACTTGCAGCCAGCTGTTGGCCACGGCCCCCTGCCCTGTGGTCTGCCGTGC
 ATCTGCTGTGCCCTCTTGTGCTGCCCTGCTGCTGCTGAGGTAAAGTGGGAGGAGGGCTACAG
 CCCACATCCACCCCTCTGCTCAATCCATAATCCATGATGAAAGGTGAGGTACAGTGCCCT
 CCCAGGCTGACTTCCCAACCTACAGCATTTGACGCCAATTTGGCTGTGAAGGAAGGAAAG
 GATCTGGCTTGTGCTCACTACAGCATTTGACGCCAATTTGGCTGTGAAGGAAGGAAAG
 TGGAGTGCAGGGGGCTCGGGCTGCCTGCTGCTGCTGCACAGAAGGCAAGTGTGGGGCTCA
 TGGTGTCTGAGACTGGCTGGACCTTGTGAGGATGGGCCCCACCTCAGAACCAACTCTG
 TCCCACTGTGGCATGAGGGCAGTGGAGCACCATCTTTGAGGGCAGAGGCGAGCGCTTTGT
 GTGTTCTGGGGAGGGAAGGAAAAGTGTGGAGGCTTTAAGTGTAGGCTTTTGAAGGAAAGG
 TTTTGTCCAGAAGGACAAGCCCGACAAATGAGCAGCTTCTGTCTCAGAGGAAGCAGGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTGTGTTCTGACGCCCTGGGGCTCTGTGCCAACG
 CCAGAGGGGCGCAGCGGACAGGCCCACTTCCACTTGTGCTGCTTGAACAGTATTT
 ATTTTGTATTTATTTGAACAGAGTTATGTCTTAATTTTTATAGATTTGTTTAAATTA
 GCTTGTCAATTTCAAGTTCAATTTTTTATTCATATTTATCTAGTGTGATGTATTC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAGGGGGCTTGGGCCCTGCAGTCACT
 CTCTCCAGAGAAATTCCTTTTGGGACTGGAGGAGAAAAGCGGCCAGGCAAGCGCCCTG
 GTCCTTTCTCTTTGGCAGTTTGGGGAAGGGCTTGGCCCCAGCTTAGGATTCAGGTTTGA
 CTGGGGGCGTGGAGAGGAGGAGGAGAACCTCAATAACCTTGAAGTGGATTCAGGTTATT
 CTGGCTGCGAGGGTTCTTTTATTTCACTTTTCTGAGTTCTCAAGGCATGAGGTGCTCT
 CACTGTGAATTTGTGGTGGCGGGGCTGGAGGAGAGGTGGGGGCTGCTCTGCTGCTCT
 CAGCCTTCTGCTGCCCTTGTCTTAAACATGCGGCCAATCGGCACCTACGTTTGCATCTC
 ATTCCACAGAAATGACCTGATGAGGAAATCTCAATAGGATGCAAGATCAATGCAAAAA
 GTTATATATGAACATAATACTGGAGTCTGCAAAAGCAAAATTAAGAAAGTAATGGACGTTAG
 AAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTCAAGCTGAAAAA
 AA

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCCTAPLDRLKVLQMVASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIQSSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIIPYAGIDLAVYETLKNWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

[illegible]

FIGURE 209

GAATTTGTAGAAGACAGCGGCGTTGCC**CATG**CGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGCGCTGC
 AGCGGGTTCATGAGCCGACCTGGGCCACGAGTTGCTACAGGAGATGAAGACCCCTCTTCTTG
 AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCCTGGCTGTGCCCATCTGTAACTCTCTGGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGGCGGACGCAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCCCTTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCTGCCCTTTCTCTGCAGCTGTTTT
 GCTTCCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG
 GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCCTCTGATTTCTGCCTATTATCCCAGGAGCAGTTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC
 AACAGTCTACCCCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG
 AGTTTTGTAACTTCAAGTGCTGTTGAGCTGCGGGGATTTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCCCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCATGGACTGCAGAACT
 CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTTGCCCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAACAGACAAAAAAAAAAAAA
 AA

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
 AATCTAATGGAACCTCCTGTCTGGGAGCCCTGGAAATGCTATGAAGAAGAAGTGTGTCT
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTT
 CAACGTGAGTAACGCCACCTGTGAGTTCCTGTCTGGTGA AAAACAAGACTCTTGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAATGTAACAGCTTAACCCCCAGCTGTCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGGTCCCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASIECPSHANTSCISSASSSSLETPVR
LYQNMFCSAENCSEETHITAFTHVHSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTHNVGSKASLYLLALASLLLRGLLP

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FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCC**CAT**GTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGCTGAATCTGGGTCCCCGGGCGGCGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATT**AAC**GAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGCCGCTCACCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGCGACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCGAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

CCGGCTCGCACCCACCGGCTGGGGGAGAAAGACGTCGCGGCGCTGGCGGCGCGGTGGTCTGCTGACTGAGGGAAC
CGCGGCTGGGAGCGGCTCCRAGGCGACAGTGAGCGGCTGACACCGACTGCATCTGCACTGGCAAGAGCA
GAATCTCTCTGGGGGGGCTCTGAATCACTTCCTGGCTCCCGCGACCAACTACATGAGCTTAGCAGGCTGGAACCT
CTGGGAGCACTGTAAATGATGATGTATCCGGTACCGCTTGGGCTTACCTCCAGGAAGTCCAAAGATGCC
CAGTTCATGACCAACTGSCCTTCTCCGGTCTCTGTTCTTTCAAGAGCGCGCATCGGCGCTGGCTCTGTTT
CATGAGCTGGCCACCTGGTGATGCTCTGCGCTACGCGACCTCTGTGGCAGCGCTCTCCCCATGTACAC
CTGTGTGSCCTTCGGCTGGTGCTGCTCAATGCATGGTCTTGCTGCACAGTCTCCACACAGGAGCACTGAC
CTCACAGAGAAATGGAATCACTCTCTGCTCCACTGATCACTCACTCAATCACTGTGCTGCTGCTCAGGAG
CTGGGGCTCGACAGCCAGCTGTGTGATGCTCTCCGGGGCTCTCTTCTGCTCATGCTGAGCTGCAGCGTCT
CTTCACTGAGCTCATCCGCTCTCGACTATGGCTACCAACTCTGTTGGCCACAGCTGGGCTATGGCGTGGTCAACTG
TGTGTGTGGCTGGGCTGGTGTCTGTGAACACAGCGCGGCTGCTCACTGCGCAAGTGGCTGGTGGTGAGTCT
TGCTGTCTGACGGGGCTCTCCCTGCTCGAGTCTGTTGACTTCCACACGCTCTTCTGGGTGCTGGATGCCATGCCA
TCTGGCACATCAGACATCCCTGTCCAGCTGCTCTTTTACAGTCTTCTGGAAGATGACAGCTGTACTGCTGT
AAGGAATCAGAGGACAAGTTCAAGTGGACGTAAGACTTGGAGCGATCTGCCCGAGTGGGATCTGCCCC
GCCCTCTGGCGTCCCTTCTCCCTCAACCTTGATGATGATTTCTCTTTTCAACTCTTGAATTTGACATGA
AGGATGTGGGCGGAAGATCTGTGGCCAGGCCACCCCTCTTGGCCCTCACCAAGCTTGGAGTCTGTTCTTAGG
AAGGCTCCAGGATCTGGAAGCTGAGATGGGACGCCCTCACTCTCTGGAGCTGAACTGGGTGGGAATGAC
GTGTGTTTCTTAGCTCTACGGGAGGAGCACTGCTGTTTCTCCCCACAGGCTCTCCCCCAATCCCGACCTGT
CTGGCTGGGCTCTGAAGGCTCTGTCTCTACTGGAGACAGGAGACACAGGCGTTAGGATACAGAGGGTCCC
CTTCTGTACACACCCCCACCTCTCCAGGACACCACTAGTGGTGCTGGATGCTGTTTCTTTCGGCAGCACA
GGTTCAAGCGGCTTCCCCATGGATCTTGAGGAGCAAGCTGCTGGAGTTGGGAAAGAGTTTCACTCTGACC
TGTGCCCTTGGCTCTCCAGGAGGCTCCACCAATCTCCCTTCAGGCGCAGGCTCAGCACAAGCCAGGCA
AGGATCTGTGCTGCTGTCTCGGTGTGAGAGCTTGCCACCTGTCTGGGAGTGTGGGCCAGGCTGAGTGATAGT
TGACAGGAGCGCTGAGCATGGGCTGGGTGTGTGTGTGAGCTCAGGCGTAGGTGGCGATGTGTGAGAGCGGTGTGT
TCGGGAGAGGAGTGTGGCTTCAAGTGTGTGTGTGACAGGGGGTGGGTGTGTGAGCTGGTGTAGGGAAGCTGT
TGCGCTGCTCTGGTGGGATGTGAGATGAGTGAATGCGGCGGAATGTGCCACAGTGTGAGAGTGTGAGACAGAT
GAGGAAATCTGTGCACATCAATAATCACTGTGAGAGCGGCACTGTGCCACAGCGCCAACTGGGCGGACGACG
CAGGAGCTCTCATGTGCCAGGCTGCCGTGTGTGATGTTCCCTGTCTGGTGCCCTTGTGCCGCCCTCTCGAAAC
CTACAGGGTCCCAACAACAGTGGCTCCAGAAAGCAGCGCCCTCGAAGACAGGAAGAAATGGGATGGC
TGGGCTCTCTCATCTCTCTTCTCTCTTCTGCTTCGATAGGTGGCCCTCCCTCCAAACCTCTCATCTCCCT
GCTGCAGCGCCCTTGCATAGCCTGATTTGGGAGAGGAGAGGGGCGATTGAGGAGAGAGGGGAGAAAGCT
TATGGCTGGGTCTGGTTTCTCTCCCTCCAGAGGGTCTACTGTTTCAGGCTGGCCCGAGGCGAGGGGGCT
ACACATGCTGTGCGCTGTGAAGAAGTGAGCTGCCATTTACAGACAGCCCTGGCATGTCTCTGCCACAGG
AATGAGATGGAGGGAGCTCCAGAAATCTTCATCCCAAGGACAGTCTCCGTTGGTGAAGCAGCATGATTATTG
CTCTGCCCTGACCCCTTGTCCCTCTTGAGGAGGAGGATGTGCTAGGACTCAACCTCAGGAGCTGGGTG
GCTCGGCTGACTGTTCTTTGATATCTGAAACTTTTAAAGTGGGAGGCTGGCAAGGGATGCTTAAATAATCAA
TTCAGAGCTCAAAAATAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRLFFQEPASAVASFLNGLASLVMLCR
YRIFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
 DAEVLEV FHP THEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNLSTEPLVKEYAAF
 VLGAAFSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGEVLAVRVVLTLLYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTCCCCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGGCTTGCCACCCCCA
 CGGGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCTCGGTGAGGCCCCACCCCCC
 TTCCCACTGACCAGCCA**TG**GGGGGCTGCGGTGTTTTTCGGCTGCACTTTGTCGCGTTTCGGC
 CCGGCCCTTCGCGCTTTTCTTGATCACGTGGCTGGGGACCGCTTCGCGTTATCATCTCGGT
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGCTTGGTTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCT
 GTCTCTGTCTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTATCAATATTTTGGCT
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTTATTACTTCTGACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCCTGGTGGTTGGGAGTCACCTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC
 TCTTGTAAGGAC**TG**ACTACCTGGACTGATCGCCTGACAGATCCCACTGCGCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTGCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCTGGGTTCAGCCAGTCACTGACTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTGTCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGACGGCCGACGGCAGGAGGACAGTCGGGTGAT
 GGTGTATTTGCGCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACAG
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTTCTAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGAGGGAGGAGGTATATTTGGAACCTTCTAACCCTCCTGGGCTATATTTCTC
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT
 GGGGGAAGGAAGGAGTGCATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTTAACCT
 CCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTGTAGTTTTTAATGGGGGTGAGGAGGGGCGGGGAGGTTTTCTATAAACTGT
 ATCATTTTCTGCTAGGGGTGGAGTGTCCATCCTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAATTTGTAAAAA
 AA

09989293.112001

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPIYYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

100211.0028660

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCCTATTANTTCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

NGTTGGAGAAAGTGGCGCGGACNNTTCATTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCG
 GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
 CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACNTG
 ACCAGCCATGGGGGCTCGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCGGCTTCG
 CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGTCGACAGGGGCA
 TTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTATCTTGGTCCATGTGAC
 CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTCC
 TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
 CATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
 TCTCTCCTTCGGTATCACGATGAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
 GGCCAGGTGTGGTTGGGATCATGGAGACTACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCGTGTCTGGTCAAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTTCGGGCCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTCAGATGCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

GGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGCCAGGAAGGCACAGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAGAGGAGG
 TGTCTGTGCGTCTCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATGG**CTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGCCGCCCATGCGAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAATGAACAGAAGAATTGTCGCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCCCTCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGGACTCGTGCTTGGGGAGATTACCTTGTGCCCCGGCCCAACAGACCCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCAACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCT**TGA**GTCA
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCACTCTCCAGCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAATGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAAGTGAAAAA

ATGGTCTCAACGACCCGGTGGGAAGACCATGGCGGGCGTGTGCCAACTTGAGGACCGGGCGCGCGGA
CAAGCCGCACTGGCGAGCTCGGGGTACGTGCTGTGACCCGTGTCTGTGGCCCTTGCTGTGTGC
TGCTGGCTGTAGCGCTGGCTGTGGCTGCTCTGTCAACCAAGCCGCCAGCGCGCGGGGACAG
CGCCGCCCTCTGCTGCTGAGCTAGCTGGGGCTGCCAGCGCCAAAGCCGCGCTTGCTACTGTGGA
AAGGCGCGACAGCTCGCACCTCGCTGAGCTATGTGATCGCGCTGCCCGACCTCACCAGCA
TCTTCGACAGCTTGAGAGAGCGCCGACGCTCTGCTGCGCGCTGCCCGACCTCACCAGCA
CAGCCAGCGCTGTGGGCGACCAAGGACAGGAGTGTGCTGCGAGCGCTGACAGAGCACCGGCC
CCGGCTGTCTGGCCGAGCTCAGAGCTGCAGACGAGATGTGCGACAGCTGGCCGACAGCTGCC
GCACGCTGGGCGCAGGGCTCAGCGCCCTGCAGAGTGCAGAGCGAGTGTGACCTACGCTCTCT
TCTGAGAGCCAGGGCCACATGCTCACTTGTAAGTCTGCTGACAGCTCTGATCTCTCT
TCAGAGGAGCCGGGGGCTGGGCGCGCCCCCAACAGGCGGACCTTCAGACAGGCGCTCTCCC
GGGGAACCGGCCCGGGGGCTGTGCATCTGCTCCGGCCCGGAGACTGTCTGAGACTCTCTC
CTAAGCGGACAGGACGAGCATGGCGTCTACTCTGTCTTTCACCCACCTACCCGGCGGCTCT
CCAGGTGTACTGTGACATGCGACAGGACGGCGGGCTGCCAGGTGTTTACGCGCCGGAGG
ACGGCTCCGTGAACTCTTCCGGGGCTGGAGCGGTACCGAGACGCGCTTGGCAGGCTCTACG
GGGAGACATGGCTAGGCTCAAGAGGATCCAGGCCCTGACCAACAGGCTGCCTTACGAGCT
GCACGTGGACGCTGAGGACTTGTGAGATGGCAGGCGCTATGCCCGCTACGGGAGCTCTGGCG
TGGGCTGTGTCTCCGTGACCTTGAGGAAGACGGGTACCCGCTACCGTGGCTGACTATTCC
GGCATCTCAGGCGCACTCCCTCTGAAGCACAGCGCATGAGTTTACCACCAAGGACGCTGTGA
CAGCGACCATTCAGAGAACAACCTGTGCGCCTTTTACCGGGGTTCCGCTGGTGATACCGAACT
GCCACAGCTGTCAACCTCAATGGGCGAGTACTCGCGGCTGCGCACGCGCTCTATGCGCAGGG
GTGGAGTGCTCTCTGAGCGGGCTGGCATCTACTCAAGTTCTCTGAGATGAAGATTCCG
CGCGGTCCGGGAGAGCGCTAGACTGGTCAAGTCTGTCTCTTGGCCCTGCTGGTGTCTGTCC
CCCCATCCCCGACCCCACTCACTCTTTGTGAAGTTCTTCCACCACCTGTGCTCTGGCGGAC
CCACTCTCCAGTAGGAGGGGCGGGGCCATCTCTTGACACAGGCTCTCCCTGGGCGGTGAAT
CACACATCGCCTTCTCGCGCTCCCCACCCTTCAAGTATTTGGACACTCACTGATCTCTTGCTC
TGCTGTAGGGGGCTGGCAACTTGTAGCCACCACCTCTGCTCTGCCCACTGTGACTCCGG
TGCTGTTTTGGCTCTCCCTGGCCAGGATGGTGGAGTGTGCCCCAGGACCCCTGTGCCCTGCC
GGCCAAATACCGGCATTTATGGGACAGAGAGCAGGGGGCAGACAGACCCCTGGAGTCTCTC
CTAGCAAGATCGTGGGGAATTCAGGTTCTCTTGAGGTAGGTTGTAGGCGAGTATCTCTCCAG
CCCTCCCAATGCCAACCCCAACCCCTTCCCTGGTGCGAGGACCAACCCCACTCTCCCCCA
GGGCTCAGCCTGGCTGTGGGCTGGGTGGGCCCATCTTACAGAGGCTGAGGTAGGATGGG
GAGCTGCTGCCTTTGGGAGCACCGCTCCAGAGGCTGAGACAGTCTCCCTGGAGGCCACCCCA
CTGTGCGCCGAGCGCTCGGGGTCTGAGTCTCTTACTCTGTGTGCCAACCCTGCTCTCTG
TCTCAATGAGGCGCAACCCATCTCCCAACCCAGCTCCCGCGCTCTCTTACTGGGCGAGC
CGGGCTGCCATCCCACTTCTCTGCTCTGGAAGTGGGTGGGGGCTGACCGTGGGGCT
GGACTGTGCACTTAATGGGAAGCTCTTGTTTCTTGCGGCTGGGGCTAGGCGAGGCTGGGATGAG
CTCTGTACAACCTGACCAACCAATTTCCAGAGGACTCAGGGTCTCTGAGGCTCTCCAGGAGG
GCTTTCTGTGATGATGCTCTGCTGAGTGGCTGTCTCCATGAGGAGAGCAACCCCTGTGCC
ATTGACCTGGGCTGACCTGCAACCGCAGGCGCGGCGGGGAGTGGTCAAGGACGAGGGA
CCACTCACCGGGCAATGSGTGTGCGGAGGCGGCACAGACCGGACCACTCTGTGTGCACACA
CTTTCTGTTGTATCTCTCCCAACCCAGCAGGCTGTCTATGCACTCTCTGTGTGCACACA
TCAGAGGTTGAACCCGAGCCTCCAGGACAGGCTGACAGGACAGGCTGAGGCGGGG
TCTCTCAGTGTCTGCTCAGGACGCTTGACCGCTGCTGTAGCTCAGGCGCGGAGGCGGG
CGGCTCTTCCAAAGCGCTCTGATGGGGCTCCGAAAGGGCTGAGTACGCTTGTGGAGTGT
GCTTACGAGCCTCTCTCTCGGCGAGGAGGGAGGTGGCTTCTCTCAAAGGACACCCGATGGCA
GGTGCTTAGGGGTGTGGGTTTCCGTTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAA
AACAATAAATTTGACTTGGCACCATCGGGGTTTGGTGGGAGGCGGTGTGACCTGGCTCTC
TGTCAGGTGCACACAGGCTACCTACATGCGCAG

MNVDRWKTMGGAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
 APPPVVSTGAASANSALVTVTERADSSHLILIDPRCPDLTDSFARLESAQASVLQALTEHQA
 QPRLVGDQEQELDLTADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
 SESQGHMAHLVNSVSDILDALQDRDLGLRPNKADLQRAPAGTRPRGCATGSRPRDCLDVL
 LSGQQDDGVYSVFPHTYPAGFQVYCDMRTDGGGWTVFQRRDGSVNFRRGWDAYRDGFGRIT
 GEHWLGLKRIHALTTQAAELHVDLDFENGATAYARYGSFGVGLFSVDPEEDGYPLTVADYS
 GTAGDSLKKGSMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSLNGLQYLRGHAASYADG
 VEWSSWTHWOYSKLFSEMKIRFVREDR

CGAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT
TGCTTCTCTGAAC TAGCTCACAGTAGCCGCGCGCCAGGGCAATCCGACCACATTTCACTCT
CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAAC TCGGCATCCAGAGCCC
CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTITTTTTTCAGTACTACC
AGCTCTCCAATACTGGTCAAGACACCATTCTC A AATGGAGAAAGATTAGGAAATACGTCC
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
TGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
AACAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
GACTGTAAATATTTCTGCCTTAGTGAAAAC TCTACCATGCTGAAGATAAACAAACAAGAAGA
CTCGGAATATTGCGCGCTGCACAGACTACTCTGAGTTTCTACTCTTATTGGACAGGGCTTT
TCCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCTACTCTGAACTG
TTCCATATATATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGCCATCTCTCAATGG
GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGCAATTCGCC
CTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCACTCTGCCTTCTTG
GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACTCCCTGTTTTCAT
GCTTCTCCTTACCTTGTGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAA
ATCCTTTTCTCTGACAGTCAAGTAGTCCATTCAGAAATTGGCAGTCACTTCCCAGATTGTACC
AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCACTACTAGTCCCTTCCCAATCCAT
CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTG
TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCACATCTCCGTTTCATATCAG
AATACCGTCCCGGATATTCCTCTCAGAGAGATTAAAGACCAAAAAAGTGAGCCTCTTCA
TCTGCACCTGTAAATAGTTTCTAGTCTCCTATTTTCTTACCATGACCATATTTATACCTTTTTCAG
GTACTGAAGATTTAATAATAATAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

230/330

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTNTTCAAGTCCAGAATATAAAGCTTGAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

CCGAGGATCGCAAGAATCTGCGCAGCCAGACAGCTGCTGGAGGGGAATCGAGGCGCGGCTCGGGGAGTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGGCCGCCCGGGGGCCGAGCCCTCCGAGTCCGCCCCCTCCGGTCCGCGCCCCCTCGGAGACTCTCTTGCTGCTCTGGGGTCTCGCCGGGGCCGGGGACCGCGCTCGGGCCGCAATGCGGGCATCTGCTGCTGCTCGTGGTGTGCGGCGCGAGGCGCGGTGGCCGCTGGGCATCTCCTGGGCTACACCTGAGCCTGCTCAGCTGCTACCTGGGTGGAGGAGCGCTCGGGCCCGCGGCCCACTCGGTGAGGACTCTGAGCTCGCGCGCGCGCAACACCAACGCGCGCGCGCCGCAACTCGGTGCAAGCCGAGGAGCGAGGCGAGGAAGCGGGGCCGAGGCGCGGGGAGAATTGGGAGCCGCGCGCTTGTCCTTACCAACCTGCACAGCCGCGCGCAGGCGCGCAAAAGGCGCTCAGGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGTTGGCGGTGCTGACCTCTCAGACACAGCTGGCCACGCTGGGCGTGGCCTGGAACCGCACGCTGGGGCACCGGCTGGAGCTGTGGTGTCTCTGACGGCGCAGGGGCCCGCGGGCCCCACTGTCATGTCAGTGGTGAACGAGGCGACCCATTTGGACACTCTGCACTGCACTGGCGCTCGGCCCACTGCTGGAGCAGCAGCGGCAGCACTTTGACGTGGTGTTCCTGTGCTGCTGACACCACTACACGAGGCGACCGCCTGGCAGCCTTACACTTGGCCAGCTCAGCCTGGCCTCGCGCCGCCACTGTACTTGGGCGCGGCCCGAGGACTCTACATCGGCGAGAGCCACCCCGCGGCGCTACTGCTACGAGGCTTTGGGTGCTGCTGTCTGCGCATGTGCTCGTACCAACTCGCCGCCCACTGGAAAGGCTCGCGCAACGACATCGTCAGTGCGCGGCCCTGCTGAGTGGCTGGGTGCTGCAATTCTGTGATGCCACGGGTTGGCTGCACTGGTGACCAAGGCGGTGCTGACATATGACCATCTGGAGCTGAGCCCTGGGAGCGCACTGCAGAGAGCGGACCTCATTTCCGAAGTGCCTGACAGCCGCCACCTGTGCGTGAACCTGTGCATGTACAGGCTGCACAAAGCTTTTCGCCGAGCTGGAACGCGACGTTACGAGAGATCCAGAGATCCAGAGTTCAGTGGGAGTCCAGAATATACCGCATCTGGCCGCTGTATGGGAGCGGGACGCTGCTTGGCCCGTGGGTAATCCAGACCATCCCGCGGCCCTCCGCGTTTGGAGTGTCTGCGCTGGGACTCTTACGAGGACGACAGCTTTCTCTCGCGCCATGGCTCACCCGCTGCCACTGCGCTGGGCTGACCGGCTGATGTGGCCGATGTTCTGGGAGACGCTGTAAGGAGCTGAACCGCGCTACACCGGCCCTTGCGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCCGACGCTTTGATCGCCGCCGGGTGATGGAATACAGCTGGACTGTCAGTGTGGAGGACATGACCCCGCAGGAGGCCCGCGCCCTCACTCGCCGAGTGCAGCTGCTCGGCCGCTGAGCCGCGTGGAGATCTTGGCTGGCCCTATGCTAGGCGCTCAGCTCTACTGTGCTGTGCTGCTTACTGTGCGGTGAGCTGACTGGCCCTGGCTTCTTGGAGGCGCTTGGCACTGTCAGCATCTGGAGCCTGGTGATGCTCGGACGCTGACCTGCTGCTATGATGAGCCGCGCAGGCCCGCGCTGGCCATGCACTGTCTTCGACCTGTCAAGGCCACGTTGGCAGACTGGAGCGCGCTTCCCGGTGCCCGGGTGCCATGGCTAGTGGCAGACAGCCCTCAACCATCGGCCCTCTATGATGCTACTCTCCAAAGACACCGCTGGACACTGTTCTCGCTGCGCGGCCACAGACGGTGTCAAGCCTGACTCTCTTGAACCGTGGCCATGTCATGCCATCTCGGCTGGCAGAGCTGTCAGGCGCTGTTTCCATGATTTCCAAAGCCTTTCCACCGAGCTGTGCCCCACCAACAGGCGCTGGGCCCAAGAGCTGGGCGCTGACACTGGCCGCTTGATCGCGAGGCAGCCGAGGCGCTGTTCTTACAACCTCCGACTACGTGGCAGCCCGTGGGCGCTGCGCGGCGCTCAGAACAAGAGGAGGCTGTGGAGAGCCTGGATGTGTACGAGCTGTCTTCCACTCTCCAGTCTGCACTGTGCTCGGGCGGTGGAGCCGCGCTGTGTCAGCGCTACGGGCGCAGAGCTGCAGCGCAGGCTCAGTAGGACTGTACCCACCTGCTCTGCAGAGCGTGCTTGGAGCGCTCGCTCCGACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGGCAACAGCAGCTGAGACCCCACTGTCCCGTGGGCGCTGGCATGGCCACACCCCACTTCTCCCCAAAAACAGAGCACTGTCCGAGCTCGTGGCAGGCTGGCGGTAGGCAGACCCAAAGCTGGCCCACTGGTCCCTCTCTGGCTCTGTGGGCTCTGGACATCTGCACTGCACTCCCAACCACTTCTTGAAGCTGCGCGAAGCTCCCTGCTCTTTAATAAACTGCCAAGTGTGGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGDDEFDFFLVPDTTYEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFERSALTAHPVRDPVHMYQLHKAFARAELERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAATLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSFLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRNTQLAMLLFEQEQQNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCCGGCAGGGCCCGCTTTTAGAAGCTTGATTTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTACCGATTCTTCTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCCTCATTGGA~~AA~~ACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCT
 TTCCCCGCCCTGAGACCTGCAGACCATCTGTCA~~AT~~GGCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGCTCTTTGGGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCGTTTGGACGCTCTGGAACATGCGACTTGCTCTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTC~~CC~~ATCATGGAATCCAAC~~T~~GCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG~~TG~~
~~ACC~~AGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

093839.1204
1021.63860

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTTGCGGCAGCGGCAGCGAGGGC
TCCGGCCGCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCAGAACCGACCACACCGTGCAAGAGGACCAGAACCCGAGGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTCTTTGGCGTCTCCATCATCCTGGTCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATCCAGAGGCCAATGGCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GC GCGCGCT **ATG** CCGCTTGCCTCTGCTCGTCTGTTGCTCCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCACGCGACAGCCTGCGGGAGGAACCTGTATCACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG
 TCCATTACAGGCTCTTTCCCAAAGCCTGGGGCAGTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCTATTCACACAAGCCTTTTGAGGACCCGATACTGGGGGCCACCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCTACTGATGTGGATAAA
 TCTTGGAAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCTTGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACCAGCTACCACTCCAGGCAGTGATATCCGCGCTGTTTGAGCAAAATG
 CACGCTGTACTAGCATCTCTTGGGAGCTGAGGCAGACCTGTCTAGTTGATTTGATGCCTTC
 ATCAGCGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAACCTTCACGGA
 GCCTTGCCCTTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTTACAACAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTATCCTAGGCAT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCATGATCAACAACCTTCGAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCAAGAAATGAGGCCCCCTCAGTGCCCTTCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAAGGGGAGCTGAGCACACTGCTGTAC
 AACCCCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACTTCCAAGGGCAAGGAGAAACAACTTACATCC
 ACTACAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTAGCTGCCG
 GCCAACTCAGTCACCAAGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCTTAACCATGGCTTCTATGTACGCCATCTGTCCTCAGCGCCCTTGTGCCCA
 GCATGTGTAGCAGCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCAGTGCACCTGTGGTGGCCGTGT
 GCTACGGCTCTCTTACAATCTCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGCCCAAGCGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**GA**TT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTCTCTCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAAGGC
 CTACAGCTGTGTGTGTCAGTACAGGAGCCACGAGCCAAATGTGGCAATTTGAATTTGAATTA
 CTAGAAATTCATTTCCTACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGGT
 GGTGCGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTTCCGCTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVKS WK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTL SVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNNLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTCCCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCTTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEgGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCTGCCTGTGGAGATGCAGGCACTGAGCCAAAGG
 CGTCCAGTGGTCCCTTGCTTCTGGCTGTCTTGGTCTCTTCTTCTCGCTTGGCCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCCACCCAAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGGCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGACAGAAAGCACCAGGGCAAAGCGGCAACCCAGCCAAAGACGCTCATTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCCAAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAG
 AGCCCCACGACGCAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAGGACCTCCAAGTCGCTGTGGTCCAGAACTCTTCTGCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGAAACACTTGGCCCAACC
 CTTTGGCTTATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGATCACTCTGT
 GCCGTGGTGGGCAACGGGGGCATCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGAGCTC
 GGACATCCTTCTACGGCTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAACCTTT
 TCTGGTTCAGGCACAGACCCCAGGAAGCTTTTCGGGAAGCCCTGCACTGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCAGTGGGGCCCTCCTGTCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGGA
 GAGAGAAGTCTGGAAGCGGGTACACGATGAAGGATAATCCGGCTGTACCAGCGTCTGGTCT
 CCGGAATGCCAAAGCCAAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGGCTGTCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGTCCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTCTGAAGTTCTTCAGTACATTTGCTGTAGTCTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCAATTCCTGCTGAAAAACACTCT
 CCAGTCCAAAGCTCTTGTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACCTCACATAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATCTAGAAGGGCTATACTTGTCTCTTG
 TCTTTAAGCTATTTGACAACCTACGTGTTGTAGAAAACCTGATATAATACAAATGATTGTT
 GTCCATGGAAGGCCAAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTEINIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGGNGQTARKLTASRTVSEKHQG
KAAATAKTLIPKQSHRLAPTGAVSTRTRQKGVTTAVIPPEKEKKPQATPPPAFPQSPTTQRN
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKAKSKSLWLQKLFPLNLTFLDSRHF
NQSEWDRLEHFAPPFQFMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGG
ILNNSHMQGEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLIILGNRGFKNVP
LGKDVRYLHFLGTRTDYEWLEALLMNTQVMSKNLFLWRHCPQAYAFREALHMDRYLLHLPDFL
RYMKNRFLRSKTLGDAAHWRIYRPTTGALLLTKLQDQVSAEFGFITEGHERFSDHYDTSW
KRLIFYINHDFKLEREVWKRHLDEGIIRLYORPGEPTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTCAGACAGACTCTTCCATAAGTCCTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

GGGCTGGGCCCCGCCGACGCTCCAGCTGGCCGGCTTGGTCTCGCGTCCCTTCTCTGGGAGG
CCCGACCCCGGCCGCGCCAGCCCCACC**ATGC**CACCCGCGGGGCTCCGCCGGGCGCGCCG
CTACCCGCAATCGCTCTGTGGTGTGGGGGCTCCCTGGTGTGCGCCGGCAGGACTGCCT
GTGTTACCTGGACCGGAATGGTCTTGGCATCGGGGTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGACGCCAGTATACCCATACCCCCAGGACCCCAAAGCTTGGCCCTGCACCCCCACAGCC
TGGCTTACATGTACCCACCTAGTGGTCTGCTCCCAATATCCACTCTACCCAGCTGGGCGCC
CAGTCTACAACCTGCGAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTTGGGGGTGGCAGGAGTCTCCAGGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCCACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACCTAGA
ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCAG
CAGGAAGGCTGGGGCCCTACTGTTTGTCCTCCTTGGGCTGGGGTGGGGGGAGGGAGGAGT
TCCGCTGACAGAGTGGCAGTACGCCCTCCTCTGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAGCTGTAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRGSHWPGFNCEFFTFC CGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGAGCTAGGCCCGGACAGTGGTGGTGGCGCGCGCAAGGTTAGGGCGGGCCACAGAA
CCCCAGGTAGGTAGACAGAGAAAGTCTGTTTCTGCCCTCAAAATGGTCCCTTGCAACCAATG
TCATTCTCTCTCTCTCTAGTTGGCTCTCTTAATCTGTGTCCACTCTCTCATGGTGTGACAG
CATGAAGACATCCCAAAACGTAGTATGGGACACCAATTTCTTTGGAAATAAAATACGACTTC
CTGATGTATCTCCAGTTCATTATGATCTCTTGATCATCGAAACCTTACCACGCTGACC
TTCTGGGAACACAGAAATAGAAATACAGCCGAGTCAGCCGCCACAGCACCATCATCTCTGA
TAGTCACTCTGCGATATCTTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
AGAACTCTGAGAGTCTGGAAACCCCCTCAGGAGCAAAATTGCACTGCTGGCTCCCGAG
CCCTCTCTGCGGCTCCGCTACACAGCTTGTCATTTCATATGCTGGCAATCTTTGGGAAG
TTTCTCGAGATTTTACAAAGACCATACAGAAACCAAGGAAGGGGAATCAGGATATACGACA
CAACACAAATTTGACCCCTGACGTACAGTAATGGCTTTCCCTCTTGATGAACCTGCTCTC
AAGAAGCTTCTGATCAAAATTTAGAAGAGAGCCAGGCACTAGGCATCTCCAATATGCC
ATTGTTGAAATCTGTACTCTGTGTCAGAGACTCATGAAGACCATTTTGATGTCTACTGTGA
AGATAGCCCTATCTCTGTGGCCCTCATCATTTTCAGATTTTGAGTCTGTGACGAGAATAAC
AAGATGGGACTCTGCTGCTTATGCTGTGCCACAGACAAGATAAATCAAGCAGATATATGC
ACTGATGCTCGCGTACTCTTTATGAAGAACTTCAGGATATTTCAGCATACCGTATCCCC
TACCCAAACAAGATTTGCTGCTCTTATGACAGCAAGTCTGGTGCTATGGAANAATCTGGGA
CTGACAACTATAGAAATCTGCTCTTGTGTTGATGACAGAAAGTCTCTGTCATCAAGGTAA
GCTTGGCATCAGACTACTGTGCCCATGAAGTGGCCCACTAGTGGTTTGGGAACCTGGTCA
CTATGGAATGGTGAATGATCTTTGGCTAAATGAGGATTTGCCAAATTTATGGATTTGTG
TCTGTGACGTGTGACCCATCTGAACTGAGTCTGAGGATCTTTGGGCAAAATGTTTGTGA
CGCAATGGAGGTAGATGCTTAAATCTCCACTGCTACAGCTGTGGAANAATCTGTG
CTCAGCTCGGGAGATGTTTGATGATGTTTTCTTATGATAAGGAGCTTGATCTGTAATATG
CTAAGGGAGTATCTAGCCCTGACGCAATTTAAAGTGGTATTTTCAGATTTTCGAGATCA
TAGCTATAAAAAATCAAAAACAGGACACTGTGGGATGTTTTCAGATTTTGGCCCTACAG
ATGGTGTAAAGGATGGATGGCTTTTGTCTAGAAGTCTCATCTACTTCTACCTCACTCA
TGGCATCAGGAAGGGGTGGATGTGAAACCAATGATGAACACTTGGCACTGCAAGAGGGGT
TCCCCTAATAACATCAGACTGAGGGGAGCAATGTACACATGAAGAGAGCTACACTATGA
AGGGCTCTGACGGCGCCCGGACACTTGGGTACCTTGGCATGTTTTCAGGATTTTGGGCT
AGCAATCAACAATGGTCCATCGATTTTGTCTAAAAACAAAACAGATGTCCTATCTCC
AGAAGAGGTGGAATGGATCAAAATTTAATGTGGGATGATGGCTATTATCATTTGTCATTTAG
AGGATGATGGATGGGACTTTTGTCTGGCTTTTAAAGGAACACACACAGACTCAGCAGT
AATGATCGGGCAAGTCTCATTAACAATGCATTTCACTGCTGACAGTTGGGAAGTCTGCCAT
TGAAGAGGCTTTGGATTTTCTTCTGTACTTGAACACTGAAATGAATATTCGGCTGTTT
AAGTTTGAATGAGCTATCTCTATGTATAGTTTAAATGGAGAAAGAGATATGAATGAAGT
GAAATCTAAATCAGGCGCTCTCATCAGGCTGTAAGGACCTCATTTGATAAGCAGACAT
GACAGCAGAGGGCTCAGTCTCAGACAAATGCTGCGGAGTGAATCTACTACTCTCCGCTGTG
TGCACAACTCATCAGCGCTGGGTACAGAGGGCAGGAAGGCTTTTACGAAGTGGAGGAATCC
AATGGAAACTTGAGCTTGGCTGTGACGCTGACCTTGGCAGTGTGTTGCTGTGGGGCCGAG
CAGAGAAGGCTGGGATTTCTTTATAGTAATATCAGTTTCTTCTGACAGTATGAGAAA
CGCAAAATGAAATTTGCCCTCTGACGAACCCAAATTAAGGAAGAAGTTCATAGGCTACTAGAT
GAAAGCTTAAAGGAGATAAAATAAAATCAGAGTTTCCAAATCTTTACACTATTGTC
CAGGAACCCAGTAGGATACCACTTGGCTTGGCAATTTCTGAGGAATAACTTGAACAAACTGT
TACAAAAGTTTGAAGTTTGGCTCATCTTCAATAGCCCACTGTAATGGGTACAAACAACTCAA
TTCTCCACAGAAAGACGGCTTGAAGAGGTTAAAGAAATTTCTTCAGCTCTTTGAAGAAATATG
TTTTCAGCTCCGTTGTGTTCCACAGACATTTGAAACATGGAAGAAAACATCGTGTGGATGG
ATAAGAAATTTGATAAAATCAGAGTGTGGCTCGAAAGTGAAGAGTTTGAACGTATGATAAGT
TTCTCCCTTCCCGGTTCTCTGTATCTCTAATCAACCAACTTTGTTGGTGTATGTTTTCAA
ACTAGAGATGGCTGTTTGTGCTCCAATCGGATATCTTTTCCCTTCAACTCATTTTGTGA
CTATCCCTGTGAAAAGAAATAGCTGTATGTTTTCATGAATGGGCTTTTTCATGAATGGGTA
TCGCTGACCATGTGTTTGTTCATCAGAGGTGTGGCCTGCAACGTAAACCAAGTGTGGGT
TCCCTGCCACAGAAATAAAGTACCTTATTTCTTCAAAAAAATAAAAAAATAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPQEQIALLAPEPLLVLGPLYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVLA
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLEFYEDYFSSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLTMEWNNDL
 WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGD
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKSGDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMEKRDMEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
 RTQNKELQLWLDESFGDKIKTQEFFQILTLIGRNPVGYPLAWQFLRKNWNKLVOKFELGS
 SSIAHVMVGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 250

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTFKNTSCDSGLGCQDTLMLI
ESGFPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGVCQETL
LLIDVGLTSTLVGTTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGGATGAGGGGAATCTGCCCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCACAGTGTCTGCCAGGGCCGCGGGGACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCGTGTCTTATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATGTGAGCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCCATAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E F G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGTCCCTAGCCAGTTCCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGTGG
 TTCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTT**ATA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
 CCTACATTAATAATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRP

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

GGCGGCTCTCCGGCTGCTCCTATTAGACTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCG
CGCGCTGTGCGCGCTGCTACCGGCTGTCTGAGACGCGGGAGACGCCAGCGAGCTGGTGATTG
GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTGC
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCTGGGTGGTGTATCCCCCTTGGGGC
TGCTGTTCTTGGTCTGCGGATCCCAGGCTACCTCTGCCCAACGTACTCTTTAGAGGAG
CTGCTCAGCAAATACAGCACACGAGTCTCACCTCCCGGCTCCGAGAGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGAGCGCCCGCTCCGCGCCGAGAGGCTGGCACCGGGGGTGGGGC
CTGGGCCACCAGCCTGCTCTGTTCCCAGCCAGCTCTGTTCCCAGCCAGTGCGTGTGATGG
CTGGCTCAGGGTCTCTCTGCGAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTTGTGTT
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGACAATCGTCACCCCTG
AAACCTTAGAGTCTCCGGGTTAAGCGATCCTGCTCAGCCTCCCAAGTAGCTGGAATACAG
CATGACCACTAGTGTGGCCAGTATAGATTTAAATATTTGTGAGATGGGGTCTTGCTACGT
TGCCACAGGTGGTCTTGAACTCTTAGGCTCAAGCAATCTCTGCTCCAGCCTCTCAAAGTG
CTAGGATTATAGGCATGAGTACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCTGCGTGGTTGCCATGACT
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
CTTTGCTAACCAGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGTCAACCTCCCAGGT
GATTGTGATGGGTGTTCCAGGTGTGGTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
TGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
GTCCTCTCTGCTCCACCAACCGGGAGCCTCCACCTTGCCATCCGTGAGTATGAATGGCTT
TTTAAACAAACCCAGCTCCCAGCCTGGGTAACTGGTAAAGCCCCGTCTCTACAAAAAATC
CAAGTTAGCTCGGCATGTGGTGTGCGACCTGATGTCACAGCTGCGAGTGGAGTGGAG
GTGGAGGTGGGGGTGGGAGTGGAGGAGGAGGATCGTTGAGCTGGGAAGTCAGGCTGCG
AGTGAGCTGAGATTGCACCACTGCACCTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTGTCTCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAAGCTTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTCAGAGCTTCATTTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCCTCCC
CTCCGATTGTTCTAAATAATTGAAAGATGCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

Q. 10. What is the difference between a strong and a weak acid?

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GAGGATTTGCCACAGCAGCGGATAGAGCAGGGAGCACCACCGAGGCCCTTGAGACATCCTT
GAGAGAGGACGACAGCATTAAGAGACCTGCCGCTTGGTGTTTTCGAGCGATGCTGGCCCTC
CGAGGAGCTTCTGCATTGCTGGTCTTGCTTTCGAGCTTTTCTGCCCCGCCGACGTTGATC
CGAGACCCGACCATGTGTGCATTACATCTACCGCGCTTTCGAGCTTCTGGAGCAGAGGGCTGG
AAAATGTACCAACAGCAGGAGGCATACATTCAAGATTTCCAAGAGTCTCAAAAATATA
TCTGTTCATTGGGAAGATGTGCAGACTCAACAAGTAGTACAAGAGTGCAGTGGGTAACCT
GGCATTGAGAGTTGAACGCTGCCAAGCGGAGATTGACTACATAACATCTTCGAGAGGCT
ACAGTGCATCGTATCAGAGGACAAGACATGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
GAGAAAAGATCGCGGACTCTCTCTGAATCGAAGCTGTGACAACATCTGTCAGGGCATAAAGT
TTTGAATAATAGTGAAGAAGATGATGACACATGGCTCTGGATGAAGATGCTGCTATATA
ACTCTCCAAAGGTGTACTATTATAATTGGATTCCAGAAACAACATGTTTGGGAATTTGCAAC
ATACGGGCATTCTAGGAGATAACCAACAGCCAGCTCCCGGGAAGCAAACTCTAACACTTTC
CTGGCGGGAACAGGCCAAGTGTCTACAAGGTTTCTATTTTTTTCAATAACCAAGCAACT
CTAATGAGATAATCAATATAACTCGAGGAAGGAGCTGTGGAAGATCAATGCTGCTCCCA
GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCTCAACTTACATTGACCTGGCTGT
GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTGTCTCA
CAAGAGTTGAGCGCGGCACACTGGGAGTGAGCAATTCAATGGGATACCCATTGCAAGAAGCAC
GATGCTGAAGCCCTATTCTCTCTGTGTGGGTTCTCTATGTGTCTACAGTATGGGGGGCA
GGGCCCTCATCGCATCACTGCATCTATGATTCATGGGCATATGAGTAGGAGGAGCACTTGC
CCAACCTGTTCTTCCCAAGAGACCAAGAAGTCACTCGATGTCATTACAACCCACAGAGAT
AAGCAGCTCTATGCCCTGAATTGAAGGAAACAGATCAATTACAACCTCCGACAAGAAGAAA
GCTGCCCTGAACTAAATGTCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC
TACAGGACAGCTGAGGCTATAGCCCTTCAACATATAGTATCCCTCAATCACACACAGGAA
AGTGTGTAGAAGTGGAAATACGTATGCTCTTCTTCCAAATGTACGTTCTTCTTAGGTATCTTC
CAAGAGCTTAGATGAGGACATATCATCAGGAAGTTTCAACATAGTCCATTACTCCCCAAA
CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGGCTACTTCAAGCCTTTTGTGTTTACT
GCTCCCCAGCATTTACTGTAATCTGCCATTCTCCCTCCCAACATTAGAGTTGTATGCGAGC
CCCTAATATTCAACCTGGCTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
CAAAATGCTATTGATATTCTCCCACTTTTCACTGCCCCAATCAAAATACATTATAATTCTTT
CTTTTCTTTTCTTTTTCGAGACAAGCTTCACTATGTTGCCAGGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCCTCTGCTCGCTCAGGCTCTCAAGTACCTGGGATACAGGCATGTGCCAC
CACACTGGCTTAAAAATCAATTTCTTATTGAGGTTTAACTCTTATTTCTCCAGTGGCTGTC
TCTTCACTAAGCTTGGTAGATGTAATATAAAGTGAAATATTAACATTGAATATGCTTTCT
CCAGTGTGAGGTTGTCACATCATGAAATCTGTTTCACTTTGTGTAACATGCACAA
TCTTTACAGCTGTCTATTCTAGAGTTTAGGTGAGTAAACAATTAACAAGTGAAGATACAGC
TAGAAAAATCACTAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
TGTTCACTTACTCTTATAGTCAATGCGTTCATGTTTCAGCCTTAAAAATATAGTCTGTCC
TTTAGCCAGTTTTCATGTCGACAGACCTTTCAATAGCGCTTTCAATGATTAATTCCTCC
AGAAAACCAAGTCTAAGGGTGAGGACCCCAACTCTAGCCCTGCTTGTCTTGTCTGCTGCTCTGT
TTCTCTCTTTCTGCTTTTAAATTAATTAAGGTGACACTGAGCTGACCAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECI VSEDKTLAEMLL
QEAEKKIRITLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFI VWLANGDTLRVFKMTKREDGGYTFTATPEDFPPK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHILKRASNESTRQLRQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAAGTGTCTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGCTTGCCCAACCTGTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCTCAGGCCCTTACGTCAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCTTAAACAACCTCCTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGCACCTGATTGAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAGAGGCCGGCAGAGGGAGGCACCTTGAGAAATGTCCTTCTCCAGGACCCAAAGTTTCTTCCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTGCTGCCCTTGGCATTGTGCTTGCCAAACACAGACGTGTTTCTGTGCCAAGCCCCAGAAAGCGGCCCTGGAGTACCTGGAGGATATAGACCTGAAACACTGGAGAAGGAACCAAGGACCTTCAAAGCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCTCTGTGCAGAGGAAGCTGCGGATCTGTCTCCTGAAAGCATGTTGGACCAGCTGGGCGTCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTCAAGAGGAGAAATCTCTCTGGATGAAAGAGAAAGATTTCTATGGTCCACAAAGCGGAAGATGTGATTTTATGGGATTTATCCGTCTGGGAGTGGTAGCACTTCTTCGAGCTGGAAACGGAGGCTTCTCTGGAACCTTGAAGGAGAAAGGCTTATCCTCTGGGGGAGTTTTCGTGGTGGGATCAGGAAGCAGGGCATTCTCTTGAGCACCGAGAAAAAGAAATTTGGAGACAAAGTAAACCTACTTCTGTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGATGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTTACTCTCAGTATGGATTTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAACCTGGGAATAGGAGGCTTAAAAATTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAGGTGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGCTCTCTATAAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGAGGCTGAGGCAGGAGAACTCACTTGAACCTGGGAGGTGGAGTTGCGGTGAGCTGAGATCAACCACCTGATTCCAGCCTGGGTGACTGAGACTCAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

0909097-11001

ACGGACCGAGGGTTTCAGGGAGGGACACGGACACAGGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCGTCGACAGTGCCCTTGGCCGGAGATGCGGTAGGAGGGCGAGCGGAGA
AGCCCTTCTCTCGGCGTGCCAAACCGGCCACCCAGCCCA**ATGG**CGCAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCGCTGGGGCCGAGCCTGGGGGCAATACA
GACCACCTTCTGCAAAATGAGAAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCTTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGCGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCCGGGCCCTCAGG
ACTCCAAGGAGACGGTGACGGGCTGCCCTGCCATC**TAGGT**TCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGTCTGTGTGACCTTGGGGAAAGGCAGTGCCTCTCTGGGCGAGTCAGATCCACCCAG
TGCTTAATAGCTAGGGAAGAAGTACTTCAAGACAGTCTGCCCTTGGAGGTCAAGAGAGGATGGG
GCTATTACTTTTATATATTATATATTAATATAGTAGTGAGATGTAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCATATGCAGTTGGCTGGACAGTTCTAAATGGACT
TTATTAATTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAATGTTGCCAAGGAAAAA

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

033323-14004
10021-6626866

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTTCAGAGGTTTGTTCCTCTTAGTTCT
 GTGCCTGCTGCACCACTCAAATCTCTCTTCAATTAAGCTGAATAAATATGGCTTGAAGATA
 TTGTCAITTTGTTATAGATCTTAGTGTGCCAGAGATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTCTTTGAAGCCACAGAAAAAGATTTTTTCAAAA
 TGTATCTATATTAATTTCTGAGAAATTTGAAGGAAATCTCTAGTACAAAAGGCGAAAAACATG
 AAAACCAATAAACATCTGATGTATAGTTGCACCACTACACTCCAGGTAGAGATGAACCA
 TACACCAAGCACTCACAGAATCTGGAGAGAAAGGCGAATACATTCACTTCACCTGACCT
 TCTACTTGGAAAAAACAAGAAATGAATATGGACCACAGGCAAACTGTTCTCCATGAGTGGG
 CTCACTCCGGTGGGAGTCTTTGATGAGTACAATGAAGATCAGCGTTTCTACCGTGTCTAAG
 TCAAAAAAAATCGAAGCAACAAGGTGTTCCGCAAGTATCTCTGGTAGAAAATAGAGTTTATAA
 GTGTCAAGGAGGCACTGCTCTTAGTAGAGCATGCAAGATGTATTTACACAAAACCTGATG
 GAAAAGATTGTCAATTTCTTTCTGATAAAGTACAAAAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCGTGTTGTAATTTGTAAACGAAAAAACCCATATACGAAGAGCTCCAAG
 CCTACAAAAATAAAGTGAATTTAGAAGTACATGGGAGGTGATAGCAATTTCTGAGGATT
 TTAATAAACACCATACCCATGGTGACACCACTCTCCACCTGCTCTCTCATTTGCTGAAGATC
 AGTCAAGAATTTGTGTCTTAGTTCTTTGATAAGTCTGGAAGCATGGGGGTGAAGGACCCCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGGAGACTGTTGAAAAATGGATCTGGG
 TGGGATGGTTTCACTTTGATAGTACTGCCACTATTGTAATTAAGCTAATCCAAATAAAGGC
 AGTGAAGAAAGAACACACTCATGCGCAGGATTAACATACATCTCTGGGAGGAACTTCACT
 CTGCTCTGGAATTAATATCATTTCTAGGTGATTCGAGAGCTACACTCCCTCTCGATGGAT
 CGCAAGTACTGCTGCTGACTGATGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGT
 AAACAAAGTGGGGCCATTCTCAATTTTATGCTTTTGGGAAGAGCTGCTGATGAAGCAATA
 AGAGATGAGCAAGTAACAGGAGGAAGCTATTTTATGTTTCAGATGAAGCTCAGAACATG
 GCCTCATTTGAGCTTTTGGGGCTCTTCAACTCAGGAAATACTGATCTCTCCGAGAAGTCCCT
 CAGCTCGAAGTAGAGGAATTAACACTGAATAGTAATGCTGGATGAACGACACTGTCAAT
 TGTATGTACAGTGGGAAGGACACGTTCTTTCTCATCATACATGGAAGCTGCTGCCCTCCGATA
 TTTCTCTCTGGGATCCAGTGGAAACATAATGGAAATTTCCAGTGAAGTGAACCTTCCAAA
 ATGGCCTATCTCAGTATTCCAGGAACCTGCAAGAGTGGGCATTTGGGCATACAACTCTTCAAGC
 CAAAGCGAACCAGAAACATTAACATTTACAGTAACTTCTCGAGCAGCAATTTCTCTGTGC
 CTCCAATCACAAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCGAGCCCAATGATT
 GTTTACCGAGAAATTTCTACAAGGATATGTACCTGTCTTGGAGCCAAATGTGACTGCTTTCAAT
 TGAATCAGAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAATGGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAATGGCAGATAT
 AGTCTAAAAGTTCTGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTAACGGCTCCACT
 GAAATAGGCCCGGTACATACAGGCTGGGTAGTGAACGGGGAAATGAAGCAAAACCCGCCAA
 GACTGAAATTTGATGAGGATCTCAGACCACTTGGAGGATTTTCAAGCCGAACGACATCCGGA
 GGTGCATTTTGGGTATCACAAGTCCCAAGCTTCCCTTGCCTGACCAATACCCACCAAGTCA
 AATCAGACAGCTTGATGCCACAGTTTATGAGGATAAGATTTATCTTACATGGGACAGCCAG
 GAGATAATTTGATGTTGGAAAGTTCAAGCTTATATCATAGAAGTAAGTGAAGTATTTCTT
 GATCTAAGAGCAGTTTGTGATGCTCTTCAAGTAAATACTACTGATCTGTGCACCAAGGA
 GGCCAACTCCAGGAAGCTTTGATTTAAACAGGAAATATCTCAGAAGAAATGCAAACTCC
 ACATATTTATTTGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT
 GCACAAGTAACTTTGTTATTCCTCAAGCAATCTGATGACATGATCCCTACACCTCTCC
 TACTCTTACTCTTCTGTATAAAAGTCATAATTTCTGGAGTTAATTTTCTAGCTGGTAT
 TGCTGTGATTGGTGGTGTGTAATTTGTTAACTTTTAACTTAAGTACACCACTTT**TGA**ACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAGAAGAGTTTAAAAAACAAACATATGTAAGT
 AAAGGATATTTCTGAATCTTAAATTTCAATTTTATTTGTTATTTGTAAGAATAAGTATGTAAC
 AAAGATCCTTTTTCATCTGATACCTGGTTGTATATTTATTTGATGCAACAGTTTCTGAAAT
 GATATTTCAAAATGCATCAGAAATTAATAATCATCTAGTATGTCAAATACAGATGAA
 GGAGAGCAAAATAAACCAACATTTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

MGLFRGFVFFLLVLCLLHQNSTSFIKLNNGGFEDIVIVIDPSVPEDEKIEIQIEDMVTTASTY
LFEATEKRFFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQFFYRAKSKKIEATR
CSAGISGRNRVYKQGGGCLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
LDKSSGSMGGKDRLNRMNQAAKHFLLTQTVENGSSWGMVHPDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSCSGIKIYAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTITVTSTRANSSVPPITVNAMKNKDVSFSPSPMIVYAEILQG
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVRAGH
GANTARLKLRPPLNRAAYIPGWVNVGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFVVSQV
PSLPLPDQYPSQITDLDATVHEDKIILTWTAPGDNFDVGKVKQRYIRISASILDLRDSFDD
ALQVNTDLSPEANSKESFAFKPENISEENATHIFIAIKSIDKSNLSKVSINIAQVTLTPIP
QANPDIDIDTPTPTPTPKDSKSHNSGVNITSLVLSVIGSVVIVNFLTSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible]

FIGURE 276

MMVMRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRFFSPI
MKVKNEKLNMAANTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIIVRTPVRGLFHLWHEKRCMDELTPEQYKCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAGAAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACC
AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCTTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
ATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT
CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCTATGGACCCATCTGTGCCCATCTG
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACACTACTGATTTTAT
CAGGGATCTGGCAACGTAGAGAAGAAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAAACATCATACCAATTTGAAATGGCATCCCTCTGATCCCTGGACATGAGAAGG
GGGCATATTAATGATGCTTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
TGTCTGCTTCTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTCTGAAATA
CCAAGAGCAGATCATATATTTTGTTTTACCATTCTCTTTTGTAAATAAATTTTGAATGTGCT
TGAAAGTGAAAGCAATCAATTATACCCACCAACACCACTGAATCATAGCTATTACAGAC
TCAAAATATTCTAAAATATTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
TAGTTATTGATTTAAGCATTTTTAGAAAATAAGATCAGGCATATGTATATATTTTACACTTC
AAAGACCTTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAAATATGGTGTAGAAATCAT
TGAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAG
TGAGAAGTAATATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAAAT
TATTCCTGTTATGACCAACACAGTGTATTATATATTTTCTGAATATCAGCCCCCTAATAGGAC
AATCTATTGTTGTGACCAATTTTACAATTTGTAAAAAGTCCAATCTGTCTAACTTAATAAAG
TAAATATCATCTCTTTTTTAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATG**T
 ATGGCAAGAGCTCTACTCGTGCAGTCTTCTTCTCCTTGGCATAACAGCTACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAAGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTCAGA
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTTGCCCTTAA
 GACACTACTTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCCCTTTCAGTATTTCTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCCTTCCACATTCTCAATTAAAAGGTGAGCTAAGCCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATTCAAACTGTTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAAGTATGAGACACATCTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
 TTTGTGC

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIVIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLETD

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FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTCATGCTTCCTGTGATTTT
ATCCAACACTACTTACCTTGCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**AATGC**
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
 GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAAA**ACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATAAAACTGAGAAAT
 GGGCCGGGCACGGTGGCTCAGCCTGTAATCCAGCACTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
 GCAGGAAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 285

GT**CATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTTGCACTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAATCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCC**TGA**ATCTGCCTGGATGGAATGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTATGCTACACACCCCTCATTTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 287

GGACAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAAGATGGACTTGTAATTGTCAT
CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAAGCCAGGA
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCATG
TAAAGTTCACAAGAAATGCTACCTTGCTTCAAGAGGTTTGAAGCATTTCATGAGGCCAATG
AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCCAGGAAGCTCCGACGAAATCAACGCC
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGGTCACGGAAGGCAAGTTTGTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
ACCGTGACAGCCTAACGGTGGCAAGCGAGAAAAGCTGTGTCTGTTCTCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCCTGTCGCAGCAGCAAGAGATACATATGCGAGTTTACCATCCC
TAA**ATAG**GTCCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAAATGCAACACAAGATCAAT
GTCCATAGCAATGATAGCATCAGCCAAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
TCTGGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
AAACAGACTAAATCTTTCTCTCTAGTCTTTCTCACTGTGACAAACCCAGTTGTGTTTTCAAA
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTTCTGTCCATGCTGGCAATAATACC
TTGTCAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCT
GCCATATCAGAACACAAACCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
TACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGATATTTGAT
CAATTTTTCATTCCCAACATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
CAAGAAGCAGATTGCATGATTAACGGAAATAGAAAAAAGAACCTACATTATTTTGCTTT
AGCATCCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCCCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATGTT
TGGAAGCTGAAAAGTGAATTTAAAGAATGCTATCTTGAAAAATTGCATACGTCGTGCAATT
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT
TAATATCAAAATACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAGCAACAATTTT
AAATATATATTTTGTCTTCAATAAATAGTGTTTAAACATGGAATGTGTTTGTGGAACAATAT
CCCACTTTTGCAAACTTACATACACATGCTTGAATTAAGTTTGTGCTGTTTTCATGCTCA
ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGDCLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQ GK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
GAGTCGGCGGGCAGGCGGGGGCCGGGACCCCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGCCCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGACGGCATCACATGAAGGTGGTGCCAAAGTCTCCTGCTCTCCGTCCCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTACAGCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCAACAAG
 CCCGGGCTCCTGCCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAACCT
 GGGCCTCTCAGAGGGGAGTTTTGCTTTCATCCACAAGGATTTTGATGTCAAAGAGACTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTCCCAAACCT
 GTTGATGAGATTAATCCTGAAACCAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCATGATGTACGGTGACGGCAAGTTTGCTCCACCTTTTGACAAGAA
 TTTTCGTGTGATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTGCTCA
 TGGAGAAAATGGGTGACCACTCGCCCTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAAACATGAAAACAGAAAACATGGAAGTTTTCTTTCCGAAGTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAAATTAC
 TGCTTATTTCCATGCCTCCTGTCTATCAAAGTGGACCGGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTCTTTGTTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCGAGCAGATGC
 CTGAAACGGTGGACAGTGTGTAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGCAGGGGAGAAATTC
 CATCTGGGTGGGACAGACAGGACGATGCAAGATTCATCCCACTACGAAATGGCATGATGGC
 TGCTTAAGACTTTAGATTGTTTATTTCTGGAATTTTTTCATTTAATGTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATTAAGGGAGGACTACTACAAA
 GCATTAATTTGATACATATTTTTTAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R I M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTCTCCC
TGTCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCC
GAGCCCACCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACCAGGGCAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAGTAGGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAGACGAATGTC
TAGTGCATTGTATGGCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGTGGACCCCTGGTGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGCTCCAGTCAGCAGGGCAGCAAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGCGGGCCACGAGCG
ATGACTACAAGAACCTTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAAACAGCATCTTATTACTCACCCATATGGCCAGCGGGAATTCCTGCGGGAT
TGTTCAAGTTCAGGGTATTTAATAACGAGAGAGAGCCAAACGCCTTGTTGTCTGGAATGAGG
TCACCCGATGTAACTGAGCATCACTGCATTGGTGGAGGAGGATATTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGCTGTTTGTATGGAGTGGAATAGGAATCATGTTGGTTA
CAGCAGCAGCGGTGAGATAACTGAGCAGCTGTGCTTATTTATCTATCGTTGAGACATTTTGTG
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACCACTTACCCA
GTAGCTAGAATGTAAATGGCAGAAGAGAAAAAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
 GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
 SAEAATSDDYKNPGYYDIQAKDLGIWHVVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
 YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN
 ALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATT
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTGGTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGLTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTMTMKPTAASNNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

0398223.112001

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCGAGCCGGAGCGCCG
TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**A**TGGCGCACCCTGTGGGGAGGC
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTCCGTGCTGCTGCTGGC
GCAGCTGTCAGAGCCGCCAAGAATTTTCAGGATGTCAGATGTAATGTATCTGCCCTCCCT
ATAAAGAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCTCT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACAGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACTGTCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
CATGTTGTCTCAGC**TAA**TGGGAATTAATTCGAAGTGATCAAGAAGAAACAGGCAGACAA
CTGGGAAGAAGTACTGGGTTTTGCTGGGTTTCACTTTTAATACCTGTTGACCTTTACCAACT
GTTGCTGGAAGATCTAAAACCTGGAAGCAAAAACTTGCTGTGATTTTTTTTCTTGTGTAACTGTA
ATAATAGAGACATTTTTTAAAGCACACAGCTCAAAGTCAGCCAAATAAGTCTTTTCTATTTG
TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAAGTCTTTACCTGGAACA
AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTG
TCGAGTTTCATTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
ACTTTTGCAGTACTGTATATCTGGGTATCTGCTGTGTCGACTTCATGGTAACGGGAT
CTAAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTAAGTGTGATGTCTGATG
CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
TGCAATAAAGAAATTTTATTTTAAAGCCAGCGCTCCCTGGATTGATAATATATACACATTG
TCAGCACTTTCCGGTCGTGGTGAGGCGACGCTTTTGAGCTCCAATATGTGCAGCTTTGAACT
TAGGCTGGGGTGTGGGTGCCTCTTCTGAAGGCTCAACCATATTGGATAACTGGCTTTTT
TCTTCCTATGTCTCTTTTGGAAATGTAACATAAAAAATAATTTTGAACATCAA

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTCCAGAGGTCTCACCTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTCAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAATACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

CCGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGAAGCGG

CCGGTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGC**CATG**TTTTGCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGT
AGACTGGACTCTGTACCAGGAGAGCAGGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
AGCAGAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAGGA
GGAGATTGTATTTCGTTACTACCACAACTCAGGATGTCTGGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATTTTCGCGAATACAGGTTCCATCATG
CTTCAAGGAGTGAGGAGTGCATGTGGAGGAACTACACTGCAGTATCCACCTAGGGAACCT
GGTGTTCAGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACAAGTGGTGAACC
CGGCAGCCCTGAGGCCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCTGTGCTCCTCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACCGAAGAAGACTAATCCAGAGATAAAA
AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAGAAATCAGAGGCCACTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCCTGTGTGTGCTCTGGGCCACTCTACCAAGTGATTTAGAGTCCCGCTCTC
CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCCCTCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAAACCAACCAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYNSLSPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKAIVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

F001-1000000

FIGURE 305

CTATGAAGAAGCTTCCTGAAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGCGGCTGGTGGCTCTGGGGATTTGGTCTGTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAAGCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAAATATGTTTGAGTTTTTGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACAGATAAGGGCTTTATGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

CCACACGCTGTCGCGCAGTTCGCGCAGTTTCTGCTCCGCTGCCAGTCTCGCCCGGATCCCGC
CCCGGGGTGTGGCGTCTGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGCGCAAGTTCGCGAGACAGCGGACAAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAATCCAGAGAGGGGCGAGAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGCGCGCGGCTATCGCCAGCTCGCTCATCCGTCTAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTACGAGCCCCAGCAAAGGCAAGACAGCTGC
GACAAAAACAGATTTAAATGCTCTTTCCGGGTCAAACCTCTCGGCTCCAAGAGAGCGCGAG
AAGAAGACAGAGCTCTAGCTTAAGGTTATAGTTACCAAGCTATACAGCGGACAGAGCTACC
ACTTGCAGCTGCAGGCGGATGGAAACCATTTAGTGACCAAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAAGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCA'TGTGAAGAAGAACACGCTGCAAGCTCATTTTCTGCTTAAACCATGAAAGTGCCATGT
ACAAGGAGCCATCACTGCAGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAATCCATGAGCCCAATGAATCAAC
GTAGCCAGTGAGGGGCAAAAGAGGGCTCTGTAACAGAACCTTACCTCCAGGTCTGTTGAAT
TCTTCTAGCAGTCTCTTCAACCAAGTTCAAATTTGTGAGTACATTACCAACCAACAGC
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGGTSCDNKLNVF SRVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEG YLYTSELF TPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLG LNK EGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSM SHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACCAAGTTGGGTTCCCTTCCCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCTGTAGATTAC
 AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAAGTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGCGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGCGCT**ATG**CGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGCCGCGTCCGG
 CGCAGCGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGCCCCGCGCGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCCGATTTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTCTACCGCCAGCGTCGTCTTGCCGGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCCTCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCACTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHTFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHLFPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

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FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCGGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATAACAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
```

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAATASGLIRQKQAREQHWDRPSASRRSSPSKNGRLCNGNLVDIFSKVIRIFGLKKRRRLR
RQDPQLKGIIVTRYLCRGYYLQMHDPDGDALDGTDDSTNSTLNLIPVGLRVVAIQGVKTGLY
IAMNAGEGYLPSELFTPECKFKESVFENYVYIYSSMLYRQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATTGAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAGGACGCAGCTTTCTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AATAAACACAGAGTTAGACCCCGGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTCCC
 CTCCCCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGAGTTTCAACAAGAAAAAGTATGTTCAATT
 TTCTCTATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTGGAAATGAAAAGTTGGGGCTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAGAGAGGAGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAAAGAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAATGACGGATAATTGCAGTTGGATTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAAACACCTGGATTTCCTCT
 GGATGTTGCTGTGATCAGTCTGAATACAACCTGTTGAATTCAGAAGGACCAACACAGATAAATTAATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTCAGGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTCTGTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTCTGT
 GCTCTGTGACCAACCACTGTCAGCAAGGTGATTTGTGTCGGAACCACTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCATAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
 GCACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGCTGCGCA
 ACCTCAACACTCTGGAACCTTTGACAATCGCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAA
 CTGAAGGAGCTCTGGTTCGGAACCAACCCCATGAAAGCATCCCTCTTATGCTTTTAAAGAAATTCCTCTTT
 GCGCCGCTAGACTTAGGGGAATGAAAAGACTTTCATACACTCAGAAGGTGCTTTGAAGGTCTGTCCACT
 TGAGTAATTTGAACCTTGCCATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAAACATAGATGAG
 CTGGATCTTCTGGGAATCAATTTATCTGCCATCAGCGCTGGCTCTTTCCAGGGTTTGTATGACCTTCAAAAACT
 GTGGATGATACAGTCCCAGATTCAAGTATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACATAATCTAACATTACTGCCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGAACCTGTAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCTC
 GAACACAGCTTGTGTGCCCGGTGAACACTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCCAGA
 ATTACTTACATGCTATGCTCCGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAATGTGCGGCCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAATGGAACAGTCATGACACA
 TGGGGCGTACAAAGTCCGGAATAGCTGTGCTCAGTGATGGTACGTTAAATTTCACAAAATGAACTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAATATCCGTTGGGAATACTACTGCTTCAGCCACCTGAAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
 GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCAC
 CACAGAGCACAAAGTCGACAGAGAAACCTTCACCATCCAGTGACTGATATAACAGTGGGATCCCAGGAATT
 GATGAGCTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGAATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAGCCACCTGCCATGCTGTCTAGCAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACACACAACAACAGTTAAACAAATAAATCAATACA
 CAGTTTCAGTCATGAACCGTTATTGATCCGAATGAACCTAAAGCAATGTACAAGAGACTCAAAATCTAAACCA
 TTTACAGAGTTACAAAAAACAACAAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAACAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKM T L H P Q Q I M I G P R F N R A L F D P L L V L L A L Q L L V V A G L V R A Q T C P S V C S C S N Q F S K V I C
V R K N L R E V P D G I S T N T R L L N H E N Q I Q I I K V N S F K H L R H L E I L Q L S R N H I R T I E I G A F N G L A
N L N T L E L F D N R L T T I P N G A F V Y L S K L K E L W L R N N P I E S I P S Y A F N R I P S L R R L D L G E L K R L S
Y I S E G A F E G L S N I R Y L N L A M C N L R E I P N L T P L I K L D E L D L S G N H L S A I R P G S F Q G L M H L Q K L
W M I Q S Q I Q V I E R N A F D N L Q S L V E I N L A H N N L T L L P H D L F T P L H H L E R I H L H H N P W N C N C D I L
W L S W W I K D M A P S N T A C C A R C N T P P N L K G R Y I G E L D Q N Y F T C Y A P V I V E P P A D L N V T E G M A A E
L K C R A S T S L T S V S W I T P N G T V M T H G A Y K V R I A V L S D G T L N F T N V T V Q D T G M Y T C M V S N S V G N
T T A S A T L N V T A A T T P F S Y F S T V T V E T M E P S Q D E A R T T D N N V G P T P V D W E T T N V T T S L T P Q
S T R S T E K T F T I P V T D I N S G I P G I D E V M K T T K I I I G C F V A I T L M A A V M L V I F Y K M R Q H H R Q N
H H A P T R T V E I I N V D D E I G D T P M E S H L P M P A I E H E H L N H Y N S Y K S P F N H T T T V N T I N S I H S S
V H E P L I R M N S K D N V O E T O I

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCGGGCACAT
 GGTGTCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCGGA
 GCGCGCCGGCGCGCCCGAGGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGG**ATG**TCCCTCCTCTCTCTCTTGTCTAGTTTCTTACTATGTTGGAACTTGGGGATCTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCGAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAAGAGGAGAGGATGAACGTCTGCCTCCCAAACTCAGGATT
 GACTACAACCCACCTGGACGAGTCTGCTGCAGAACTTTACCATTGCTTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAAGTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGCAGGCAATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT
 CCTCTTCCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCCTCACTCGCTCCACAGCAAA
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGTCT**TGA**ATTACAATGGACTTGACTCCACAGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTCTTATACAAATACCAACAAAGCAAA
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAGGTTG
 AGGTGAATATACCTAAAATCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATTT
 TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTTCAGACAGTCAAGCAGAAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCAAGAACTCCAAAAAGGAAACATGTGCTTCTATTCTGACTTAAC
 TTTCAATTGTCATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTGATTGAGCCCAAAATAAC
 TATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGACTTTPCACTTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTTCAAA
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCAAT
 TATCAAGCTCTCTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATT
 CCCAACATACCATATAGTCTCTTCTTCTGAGAAATGTGAAACCAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTCTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGCACTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLTHTTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQFGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGGAGCGCGCGGGGAGGCTCGGGACAGGAGCGAGACGCGCTACTCGACGCGCGGCCACGCGGACCGGAGGCCA
CGGCGCGCTCTCTGCTGCTCTGCTCTGCTCTCTGCGGAGTAGGTGATTCGCGAGACGTTTGGATATCACTACT
CCTGAAAGATGATTTGAAAAGAACCAAGGGGAAACTGCCATTGCCGATCAAAATTTACGCTTTAGTCCGCGAAG
CAGGGAGCGCTGGACATCGATGGCTGATATCACCAGCTGATATCAAGAAGTGATCACTGATGATTATTTAT
ATTCTGGAGACAAATTTATGATGACTACTATCCAGATCTGAAGGCGGAGTACATTTTACGAGTATGATCTC
AAATCTGGTGATGCTCAATAAATTAACGAATTTTACAACCTGCAGATATTGGCACATACAGTGCAGAAATGAA
AAAAGCTCTCTGCTGTTGCARAATTAAGAAGATTTCATCTGGTAGTCTCTGTTAAGCGCTTCAGGTCGAGATGTAC
TTGATGGATCTGAGAAGATTTGGAGATGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACCA
TATGATCGGCGAAAATTTGCTGACTACAGAAAATGCCCACTCATGGTATGACAGAAATGACTTCACTGTTGAT
ATCTGTAAAAAATGCCCTTCTTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGGATGGGGCTGTGATC
AGTGGCTTCTGCGTCTAAAGCTTGTCCCTCTCTCAATAAAGCTGGAGCTAATTCGAGGAGCATATTAGGAAGT
TTGCTTGTCTTAGGCGCTATTGGTCTTATCATCTTTTGCTGTCTGTAAGAAAGCGCAGAGAAAGAAAATTTGAAA
GGAAGTTCATCAGCAATCAGGGAAGATGTGCCACTCCAAAGAGCGGTACGTCACCTGCCAGAGCTACATCG
CGATTAAGTCAATCATCTCCTGGGCGCCATGTCTCTCCAACTGGAAGGATATTCACAGACTCAGTATAACCA
GTACCACTGGAGACTTTGGAACGCATCTCCAGAGCTCCGACTTCCCAAGCTGTAAGTTCAAGTACCCITACA
GATGATGGAATACAGTTGATGATAAGTACTGAGAAGATCTGAAGTATGTGATTTATGCTATTTGCTATTT
AGGCGCTTAGTAAGAGCTATAAGTTGTTTTTAAAAAAGACAGGCAAGACAGATATAGACGAGCTGTAGAACAC
ATCTCACTTTATGCAATGGCATAGACATGTAGTTCAGAGTCACTGCTCAAAATAGTAGACGAGCAGAAATTTCTTGT
TAAAAAACCCCTATGTATAGTATGACATGATAGTTAAAGATGTTTTATTTATTTTCAATAACTACCTAACAA
ATTTTTAACTTTTCATATGACATATTCTGATATGGTCTTTAGGAAAAGATATGGTAAATGATTTATTTTCA
AGAAAATTTAAAAATCTTACGTTCTTTTAAAGTTTGTGCTAATAGTTAAATACATGAAGGGAATAACCCG
CTCTTTTCCGCTTTTATGACACACACAGGACAGCGGTTGTCATGCTCAAACTCTTTTATTTTGAACATCA
TGATTTACACAAATTTCTTTTAAACACAGACATAAAATAGATTCTCTGTATATAATAACTTACATACGCTCCA
TAAAGTAAATTTCAAAGAGTGTGACAAACAAATGCCACTCTACAGTGTCTCTGCTCAAACAGAGTGATGC
ACAAATATAATAACTCAAGTCCAAATATAAAACCTAGGCACTTGACTAACTTAAATAAATTTCTCAAACTA
TATCAATATCTAAAGTGCAATATTTTAAAGAAAGATTTCTTCAATAACTCTATAAAAAATAGTTTGTATGG
TTTGGCCCATCTAACTCTACTACTATTAGTAAGAATTTTAACTTTTAAATGTGTAGTAAGGTTTATCTACCTT
TTTCTCAACATGACACCAACACAAATCAAAACAGAGTTAGTGGGTGCTACAGTGTGAGGATTAATCCAGTG
TCGGGTCACAAATGCAATTCAGAGGAGGATACCCATCTGCACTGGAAATGGGCGATATGTTTTTTTCTCTCC
TGATTTGTGATAACCAATGGAGCAGGAGGAGGATGTAGTTCTGATGCCATTCCTCGATACATCTCTGCTCT
TTTCTGGGCAAGGGTGCCCAATTTGGAAGAGGTGGAAATATAGTTTCTGAAATCTGTAGGGAAGAGACACAT
TAGTTAATTTCTAAGGAAAATAATCATCTATGTGTCCAGATTCTCATTAAGACAAATGTACCCACAACT
GAGATCACATCTAAGTGACACTCTTATTTGCAGGTCATAACTATAAAACCTCATGTGTAATAGGCGTATA
TGTTAATACAGTGGACCAATTTCTTGATGCTATAAGAAATTAATAAACTCAAAACGACTCTTCTTAAACAA
CTTCAACCAAAAAAGACAAAACATGGAACGAGGTGAAGCTTTGAAGACATCTGTTTGTATGTCAGTGGTTT
CCACGCTGGCTAGGACGAGGCTCACTTGGAGCTTTTAAATACAAACAACTTGGAGTGGAGGCCATTTCTCT
AGCAAACTAATCGGAAGACGAAATCACTTACCGCATTTCTCACTTTTAAAGTGGGAGGTAAATGATAGAAGT
TATGAACACAAGAGGAACATAGACATTTGGAGTCTATTTGAGAGGCGGGTGGGAGAGGAAAAGGACA
GAAAGATGAACATTTAGATAGTGCCTTCCACACTGGGTGATGAATTAATGTACACAAATCCCTGTGACACA
TGTTTACCTATGGAACAAACCTCTATGTGTATCCCTAATCACTATAATTAAGAGTTTAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 318

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><subunit 1 of 1, 352 aa, 1 stop
```

MALLLCFVLLCGVVDFARSLSITTP EEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVILILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVLVLPKPSGARCYVDLGSSEIGSDFKICEPKEGSLPLQYEWQKLSDSQKMP
SWLAEMTSSVIVSKNASSEYSGTYSCTVNRVRNGDQCLLRNLVPPSPNKAGLIAGAIIGTLL
ALALIGLIIFCCKRRKREEKEYEHVHDIRVEDVPPKSRNSTARSYSIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSDEFERTPOSPITLPAKFKPYKYTDGITV

amino acids 1-19

amino acids 236-257

amino acids 106-110, 201-205, 298-302

amino acids 31-39, 78-85, 262-270

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
ATGGTGAAGGTGCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTGTGTGCTCCCTTGCTGGGTTTTACCCTG
CTTCTCTGGAGCCAGGTATCAGGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
GAAGGGGGTGTGCCCAAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCCTCGGAT
GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAA
CCACCACAATAGAACAGCTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACT
TGTGTTCTCATGTCGTACACTGCAACCCAGTCACAAGAAATGAGATGTTTTCCATCAGAGAC
AGTGCTCAGCAGGGCGTTTCTGCTATTCCGAGAGAGCAATCAAACAGTTGGACGTAGAAGCAGC
TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTACAAGC
TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTGTGTTGCCCTGTGTCATTTC
AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCCTCGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTATTACAACCTCTATT
AATTAATGTCAGTATTTCAACTGAAGTTCATTATTATTGTGAGACTGAAGTTACATGAAG
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTACAATCCTGCCACAGTGTGGGCGAG
TGGATGGGTGCTTAGTAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACTTCAGAGCATGAAAATCACACT
GTCCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCACTGTGTTGAAAAG
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
TCCCACCCACACTCGCCAGCTCACCCATCATCCCTTCCCTTGGTGCCCTCCTTTTTTTTT
TATCTTAGTCATTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
ATTGCAACCTGGATGACTATCCAATCTGTGATGACATTCCCTGCTAATAAAGACAACATAA
CTCCAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARPCPLLATASQMVMVLPCLGFTLLLSQVSGAQQGEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCCGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGCTTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTTGTAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAAGAGTAGCAGTAAGTACCGCCTATAGAGTCTATAGGCCACTTGGCTTCGTTAG
AACCGGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCTTTCTCTCCACAGGTGTCCACTCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGATGTTGGGGGCCGCTT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGTGGGGTGGCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACTCTGCATGGATTTTCAAGGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTTACCACCTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACC
CACCCCCGTACTCCAGTTCTCTGTCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
CTGAAGCCCCGGGCCCGATGACCCGGCCCCGGCTCTCTGTTACAGGAGCTCCCGAGCG
CGCAGGACAACAGCCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTCGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHENTPIPRRHTRSAEDDSE
RDPLNLVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

GGTAAAGGTATCCCGCAGAGACAGCCAGCAGTCTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCGCTCTGGAACCTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAACATCTCCAACTTCATGTGTC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGTATCCCGAGGAAGCCATCTTTGACACCCTTTGACCCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCAT
GGTCCCGGGGATGTATGTCCTCTCTCGTGAAGCCCTGGTGACTGTCAAAACATCGAG
GTTATTAAATGCAAGCATCAGAAATAGAAACAACAATCTCCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCAGGAAGGGGTGAAGCGCTCGTCCACTCCGATCCACGAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCATAGGTCAGAGTACAGCCTCTGCCGAGACCTGTCC
ACAGCCGGCACCCAGAGTCACTGTCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACGAGTGGGCAAAACAACCTTC
CTTGTCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCACCAGCAGGGACCTT
CTTCTCTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCAAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGAC**TGA**TGTCAGGTGAAATGAGGTTTCTCTCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGAGCTCCAC
CGGGAACCTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTTAGCCTG
GGCCCCCACCAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
CGGAGTGTATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CAGATGTTCTGTGTTTCAGTGAAGAGAGACCTGATCACCATCTGTGTGCTTCCATCTGCA
TTAAATTCACCTCAGTGTGCCCAAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGFSTRADTAMTTDDTEVPAMTILAPGHALETQTLSA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPGAGM
TTVQTTITGSDPEEAI FDTLCTDSS EEA KLTMDILTLAHTSTEAKGLSSESSASSDGPHFV
ITPSRASESSASSDGPHFVITPSRASESSASSDGPHFVITPSWS PGSDVTLTAAEALVTVTNI
EVINC SITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPNTSARETAVTAPGATTLTSGALVTVSRNPLEETSALS VETPSY
VKVSGAAPVIEAGSAGVKTTSFAGSSASSTAGSEALLKNFTPSRPTMDIATKGFPTSRD
PLPSVPPTTNSRGNTSLAKITITSAKTTMKPOOPRPLRPGRGPOT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTCGCCGGTCTCTCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGAG
 CTTGACTTACACTTTGGTAATAATTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGCACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTCTGTGCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTTCTCTTTACATGGCCAATTTTCAACAAGCAGTCACCTCCCC
 TAGCCCATCATCACACAGATTATTTCAAAGCCCAACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAAAATGTGAGTGCGCTCCAGCTACGGTGCGAGTTGCTTCTCCA
 CATACCACCTCGGTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCATTCTC
 AGCCTCCCACGACCTCATTTCTACAGTTTTTACACGGGCTCGGGCTACATCCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTACAGCACCCTACGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAAATCAGTACGGGCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCTCGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGCTCTTAAATCAAT
 TAGTAACCAAGAGCCCAATGAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAAGTACGATCTCGGCTCTCACCACCACTCCGCTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTGACCTAGTGTATCCACCTCTCGGCTCCCAAGTGTCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGTAAGTGT
 GGAACCAAAATAGGTAATTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAGCTCT
 ATGTAAAGTAATAAGTATAATTGCCATATAAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCCTGGTTCAGATAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAATCTTATT
 CCAGATGTAGTTTCTTCCAATTAATATTTGAATAATCTTTTGTACTCAA

FIGURE 328

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVLIICFLTRLSASQNCCLKSLEDVVIDIQSSLSKGIKRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIHLLENVVSALPATVAVASPHSTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCAGGTTGTCAGCGCCAGAA**ATG**CGGCTTCTGGTCTGCTATGGGGTTGCCGTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCTTGCAGTGCACCTACAGGGAGAGCTGAGGGACCACCGGAAGTACTGGTCAGGAAAGGGT
 GGGATCCTCTTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAAGAGGCCAGGAGCAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGTCTATTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCCTGCAGGCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTGGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCTGCAGGGAGCTCCCGCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCAGTGTCCGCATACTGGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTACGC
 CGCAGGCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAAGCTCAACAGGCCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTCGGAGGAAAGAGGCC
 CCTTCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCCTCCCTCCACATCTTGAGGAGGA
 GCTGGGCTTCTGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAACGATATTGGCTGGCTGGATCAGCACCCGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGTGTCCCGGACTCCAGGGCTCTCCCCACCTCCCGAGGCTCTCCTTGGATGTTCCTCA
 GCCTGACTCAGAAGCGTTTGTGAGCCTGGAGCCAGCCAGCTGGGCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTCATGGCCAGTGTGCGACCCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGTAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCCAGGAAGCCT
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGAC
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCGACTTGAGTTTGGGGCCAGTGGGCCTG
 ATGAACGCTCACACCCCTTCACTTAGAGTCTGCACTTTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCTTTNCCATTGGCCCTCCTGNNCCATGCCCTTCTGCTTTGGAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAGAGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAAGTAAAAAACCCAGGTGCAGTGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTGGAGAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACCTATATTTTTTCTTTTCCATTATATTGTTTTTAAAGACAGAATCTCGTGTCT
 GCTGCCACAGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCTCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCCTGAC
 CTCAAATGAGCCCTCCTGCTTCTCAGTCTCCAAATTGCGGGATTACAGGCATGAGCCACTGT
 TCTGGCCCTATTTCTTTTAAAAAGTGAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCAACCATAGTCTACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGAGCAATATCTGTATATACAACCTTTGTATCCTGCCCTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196.

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSTRQELSLIVTLWNLTLDAGEYWCWVEKRGPDSELLISLFV
FPGPCCPPSPSPFTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWSRLTAEKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128